



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165896

TO: Nita M Minnifield
Location: REM/3C01/3C18
Art Unit: 1645
Saturday, September 17, 2005

Case Serial Number: 10/002784

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
9-05*

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STIC-Biotech/ChemLib

165896

From: Minnifield, Nita
Sent: Thursday, September 15, 2005 4:51 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

10/002784

STIC

Please do a commercial and interference sequence search on SEQ ID NO:16 and 27 of this application.

Please provide a paper copy of all results.

Thanks,
Minnifield
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

RECEIVED
SEP 15 2005
STIC-BIOTECH/CHEM. DIVISION
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 9/16/05
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search: _____
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: DS
WWW/Internet: _____
Other (Specify): _____

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RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61554; CAA43752.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >220 type A exotoxin.
FT NON_TER 220 220
FT SEQUENCE 220 AA; 25600 MW; 92DB096E57906DF6 CRC64;

Query Match 41.1%; Score 1027.5; DB 2; Length 220;
Best Local Similarity 98.0%; Pred. No. 1.4e-58;
Matches 194; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 61
Db 23 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 82

QY 62 ELKQEMATLFKDKNIDYGVYHYHLCYLCEAERSACI-GGVTRNREGNHLIPIKKIVVK 120
Db 83 ELKQEMATLFKDKNIDYGVYHYHLCYLCEAERSACIYGVTNHEGHNHLIPIKKIVVK 142

QY 121 VSIDGIQSLSPDIETNKGWVTAQELDYKVRKYLTDNKLQYTNKQYTGPKSYETGYIKFIPKNKE 180
Db 143 VSIDGIQSLSPDIETNKGWVTAQELDYKVRKYLTDNKLQYTNKQYTGPKSYETGYIKFIPKNKE 202

QY 181 SFWDFPFPEPEFTQSKYL 198
Db 203 SFWDFPFPEPEFTQSKYL 220

RESULT 12
ID Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61573; CAA43771.1; -.
DR PIR; S18789; S18789.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

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DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
FT SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 39.5%; Score 986.5; DB 2; Length 236;
Best Local Similarity 88.2%; Pred. No. 6.9e-56;
Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 61
Db 23 QQDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 82

QY 62 ELKQEMATLFKDKNIDYGVYHYHLCYLCEAERSACI-GGVTRNREGNHLIPIKKIVVK 120
Db 83 ELKQEMATLFKDKNIDYGVYHYHLCYLCEAERSACIYGVTNHEGHNHLIPIKKIVVK 142

QY 121 VSIDGIQSLSPDIETNKGWVTAQELDYKVRKYLTDNKLQYTNKQYTGPKSYETGYIKFIPKNKE 180
Db 143 VSIDGIQSLSPDIETNKGWVTAQELDYKVRKYLTDNKLQYTNKQYTGPKSYETGYIKFIPKNKE 202

QY 181 SFWDFPFPEPEFTQSKYLMIYKDNETLDSNT 211
Db 203 TFWDFPFPEPEFTQSKYLMIYKDNETLDSNT 233

RESULT 13
QY38P4 PRELIMINARY; PRT; 222 AA.
ID Q938P4;
AC Q938P4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=12620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
RL FEMS Microbiol. Lett. 219:291-295 (2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1

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RN
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS165, MGAS327, MGAS493, MGAS494, MGAS167, and MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RT Nelson K., Schlievert P.M., Seldander R.K., Musser J.M.;
RA "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61560; CAA43758.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 43.8%; Score 1095.5; DB 2; Length 236;
Best Local Similarity 98.1%; Pred. No. 6.4e-63;
Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
DB 23 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
QY 62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIKKIVVK 120
DB 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIVVK 142
QY 121 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 180
DB 143 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 202
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNT 233

RESULT 10
Q57453
ID Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, MGAS250, MGAS256, MGAS285, MGAS480, MGAS492, and
RX MEDLINE=92044323; PubMed=1940804;
RT Nelson K., Schlievert P.M., Seldander R.K., Musser J.M.;
RA "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61560; CAA43758.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 43.8%; Score 1095.5; DB 2; Length 236;
Best Local Similarity 98.1%; Pred. No. 6.4e-63;
Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
DB 23 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
QY 62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIKKIVVK 120
DB 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIVVK 142
QY 121 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 180
DB 143 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 202
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNT 233

RESULT 10
Q57453
ID Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS165, MGAS327, MGAS493, MGAS494, MGAS167, and MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RT Nelson K., Schlievert P.M., Seldander R.K., Musser J.M.;
RA "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR EMBL; X61567; CAA43765.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; 2EF7F41AAC853600 CRC64;

Query Match 43.6%; Score 1089.5; DB 2; Length 236;
Best Local Similarity 97.6%; Pred. No. 1.6e-62;
Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
DB 23 QDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
QY 62 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACI-GGVTNREGNHLIPIKKIVVK 120
DB 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIVVK 142
QY 121 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 180
DB 143 VSIDGIQSLSFDIETNKKMVTQAQLDYKVRKYLTNKKLYTNGPSKYETGYIKFIPKNKE 202
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNT 233

RESULT 11
Q79AQ0
ID Q79AQ0 PRELIMINARY; PRT; 220 AA.
AC Q79AQ0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
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RESULT 7

Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS485, MGAS158, MGAS491, MGAS495, and MGAS624;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61569; CAA43767.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR EMBL; X61572; CAA43770.1; -
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1 Potential.
FT SIGNAL <1 22 type A exotoxin.
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 43.9%; Score 1096.5; DB 2; Length 236;

Best Local Similarity 98.6%; Pred. No. 5.5e-63;
Matches 208; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 QQDPDPSQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
DB 23 QQDPDPSQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
QY 62 ELKQEMATLFDKKNIDYGVVEYHLYCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
DB 83 ELKQEMATLFDKKNIDYGVVEYHLYCYLCENASACIYGGVTNHEGNHLEIPKIVVK 142
QY 121 VSIDGIQSLSFDIETNKKQVTAQELDYKVRKYLTDNKKLYTNGPSKYETGIKFIPIKKE 180
DB 143 VSIDGIQSLSFDIETNKKQVTAQELDYKVRKYLTDNKKLYTNGPSKYETGIKFIPIKKE 202
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNT 233

RESULT 8

Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Besen D.E., Izso M.W., Fiorentino T.R., Caringal R.M.,
RT Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636 (1999).
DR EMBL; AF055698; AAD11624.1; -
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 43.8%; Score 1095.5; DB 2; Length 222;

Best Local Similarity 98.1%; Pred. No. 5.9e-63;
Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 QQDPDPSQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
DB 11 QQDPDPSQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 70
QY 62 ELKQEMATLFDKKNIDYGVVEYHLYCYLCENASACI-GGVTNREGNHLIPIPKIVVK 120
DB 71 ELKQEMATLFDKKNIDYGVVEYHLYCYLCENASACIYGGVTNHEGNHLEIPKIVVK 130
QY 121 VSIDGIQSLSFDIETNKKQVTAQELDYKVRKYLTDNKKLYTNGPSKYETGIKFIPIKKE 180
DB 131 VSIDGIQSLSFDIETNKKQVTAQELDYKVRKYLTDNKKLYTNGPSKYETGIKFIPIKKE 190
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNT 211
DB 191 SFWDFPFPEFTQSKYLMYKDNETLDSNT 221

RESULT 9

Q9R931 PRELIMINARY; PRT; 236 AA.
AC Q9R931;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;

```

RESULT 6
SPEA_STRPY
ID SPEA_STRPY STANDARD; PRT; 251 AA.
AC P62560; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12.";
RL Infect. Immun. 52:144-150(1986).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B.";
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors.";
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
-----
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-----
CC EMBL; U40453; AAC48868.1; -.
CC EMBL; X03929; CAA27568.1; -.
CC PIR; A26152; A26152.
CC PDB; 1B12; X-ray; -.
CC PDB; 1FNU; X-ray; -.
CC PDB; 1FNU; X-ray; -.
CC PDB; 1FNW; X-ray; -.
CC PDB; 1HA5; X-ray; -.
CC PDB; 1HA5; X-ray; -.
CC PDB; 1LOX; X-ray; -.
CC InterPro; IPR008992; Bact_endotox.
CC InterPro; IPR006177; Bctrl_tox.
CC InterPro; IPR006123; Stap/Strep_toxin.
CC InterPro; IPR006126; Staph/Strep_tox.
CC InterPro; IPR006173; Staph_tox_08.
CC Pfam; PF02876; Stap_Strp_tox_C; 1.

DR Pfam: PF01123; Stap_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Signal; Toxin.
FT SIGNAL 1 30 Exotoxin type A.
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18 K -> E (in Ref. 2).
FT CONFLICT 25 35 VT -> MK (in Ref. 2).
FT CONFLICT 40 40 SOEFAQODPD -> LPKGICSTRPK (in Ref. 2).
FT CONFLICT 43 43 H -> Q (in Ref. 2).
FT CONFLICT 47 59 S -> N (in Ref. 2).
FT CONFLICT 47 59 NLQNIYFLYEGDP -> TPKIYIFFMRVTL (in Ref.
FT 2).
FT CONFLICT 129 129 I -> L (in Ref. 2).
FT CONFLICT 165 178 TNKKWVTAQELDYK -> QIKNGNCSRIYSVT (in Ref.
FT 2).
FT TURN 36 38
FT HELIX 42 44
FT TURN 46 48
FT HELIX 49 56
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 102
FT TURN 103 103
FT STRAND 106 110
FT STRAND 113 113
FT TURN 115 116
FT TURN 121 122
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 186
FT STRAND 197 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 251
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4C0CCBFCC3 CRC64;

Query Match 45.2%; Score 1129; DB 1; Length 251;
Best Local Similarity 97.7%; Pred. No. 4.7e-65;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 2 QODPPSQLRHSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLSHDLIYNVSGPNYDKLKT 61
Db 31 QODPPSQLRHSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI -GGVTNREGNHLIIPKKIVVK 120
Db 91 ELKQEMATLFDKKNVDYGVVEYHLCYLCEAERSACI YGGVTNHEGNHLIIPKKIVVK 150
QY 121 VSIDGIQSLSEFDIETNKKQVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFPKNKE 180
Db 151 VSIDGIQSLSEFDIETNKKQVTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFPKNKE 210
QY 181 SFWDFPFPEPEFTQSKYLMYKDNFTLDSNT -QIEVYLTTK 220
Db 211 SFWDFPFPEPEFTQSKYLMYKDNFTLDSNTSQIEVYLTTK 251

```

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OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
DR EMBL; AB014161; AAM79908.1; -.
DR EMBL; AP005142; BAC63655.1; -.
DR PIR; A60108; A60108.
DR HSP; P01552; LSEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;

Query Match 45.2%; Score 1130; DB 2; Length 251;
Best Local Similarity 98.2%; Pred. No. 4.1e-65;
Matches 217; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 2 QDDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 61
DB 31 QDDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

QY 62 ELKQEMATLFDKKNIDYGVYHYHLCYLCEAERSACI-GGVNREGNHLIPIKKIVVK 120
DB 91 ELKQEMATLFDKKNIDYGVYHYHLCYLCEAERSACIYGGVTHNEGNHLIPIKKIVVK 150

QY 121 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 180
DB 151 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 210

QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
DB 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 5
ID SPEA_STRP8 STANDARD; PRT; 251 AA.
AC P62561; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

```

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DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA; OrderedLocuaNames=speyM18_0393;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS832 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic fever
CC (By similarity).
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC
CC EMBL; AE009982; AAL37141.1; -.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome; Signal; Toxin.
FT SIGNAL 1 30 By similarity.
FT CHAIN 31 251 Exotoxin type A.
FT DISULFID 117 128 By similarity.
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCBCFCC3 CRC64;

Query Match 45.2%; Score 1129; DB 1; Length 251;
Best Local Similarity 97.7%; Pred. No. 4.7e-65;
Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 2 QDDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 61
DB 31 QDDPPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

QY 62 ELKQEMATLFDKKNIDYGVYHYHLCYLCEAERSACI-GGVNREGNHLIPIKKIVVK 120
DB 91 ELKQEMATLFDKKNIDYGVYHYHLCYLCEAERSACIYGGVTHNEGNHLIPIKKIVVK 150

QY 121 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 180
DB 151 VSIDGIQSLSPDIETNKKQVTAQELDYKVRKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 210

QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
DB 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

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RL Microb. Pathog. 15:327-346(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A-20 / Serotype M1,T1;
RA Wu J.-J.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Sv / Serotype M23;
RA Hong K.;
RT "A novel cloning method used arbitrarily primed PCR.";
RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071593998;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Prineas C., Sezate S., Suvarov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Bersis S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RN Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okazashi N., Kawabata N., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution";
RN Genome Res. 13:1042-1055(2003).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Rickiells S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RN Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [9]
RP PRELIMINARY SEQUENCE OF 28-86 AND 121-398.
RA Yonaha K., Elliott S.D., Liu T.-Y.;
RT "Primary structure of zymogen of streptococcal proteinase.";
RN J. Protein Chem. 1:317-334(1982).
RN [10]
RP PRELIMINARY SEQUENCE OF 146-398.
RX MEDLINE=76190087; PubMed=1270417;
RA Tai J.Y., Kortt A.A., Liu T.-Y., Elliott S.D.;
RT "Primary structure of streptococcal proteinase. III. Isolation of
RT cyanogen bromide peptides: complete covalent structure of the
RT polypeptide chain.";
RN J. Biol. Chem. 251:1955-1959(1976).
RN [11]
RP FUNCTION.
RC STRAIN=NZ131 / Serotype M49,T14;
RX MEDLINE=99081733; PubMed=9864206;
RA Kuo C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T.,
RA Lin Y.-S.;
RT "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces
RT phagocytic activity in U937 cells.";
RN Infect. Immun. 67:126-130(1999).
RN [12]
RP FUNCTION.
RC STRAIN=A-20 / Serotype M1,T1;
RX MEDLINE=99386817; PubMed=10456871;
RA Tsai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;
RT "Group A Streptococcus induces apoptosis in human epithelial cells.";
RN Infect. Immun. 67:4334-4339(1999).
RN [13]
RP FUNCTION.
CC -!- FUNCTION: Important streptococcal virulence factor which cleaves
CC human fibronectin and degrades vitronectin. Also cleaves human
CC IL1B precursor to form biologically active IL1B. Can induce
CC apoptosis in human monocytes and epithelial cells in vitro, and
CC reduces phagocytic activity in monocytic cells. Thus, may play a
CC role in bacterial colonization, invasion, and inhibition of wound
CC healing.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic
CC residues at P2, P1 and P1'.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the peptidase C10 family.
CC
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CC EMBL; M86905; AAA26978.1; -
CC EMBL; L26125; AAA26979.1; -
CC EMBL; L26126; AAA26992.1; -
CC EMBL; L26127; AAA26993.1; -
CC EMBL; L26128; AAA26994.1; -
CC EMBL; L26130; AAA26996.1; -
CC EMBL; L26131; AAA26997.1; -
CC EMBL; L26132; AAA26998.1; -
CC EMBL; L26133; AAA26999.1; -
CC EMBL; L26134; AAA27000.1; -
CC EMBL; L26135; AAA27001.1; -
CC EMBL; L26136; AAA27002.1; -
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CC EMBL; L26141; AAA27007.1; -
CC EMBL; L26142; AAA27008.1; -
CC EMBL; L26143; AAA27009.1; -
CC EMBL; L26144; AAA27010.1; -
CC EMBL; L26145; AAA27011.1; -
CC EMBL; L26146; AAA27012.1; -
CC EMBL; L26147; AAA27013.1; -
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CC EMBL; L26149; AAA27015.1; -
CC EMBL; L26150; AAA27016.1; -
CC EMBL; L26151; AAA26980.1; -
CC EMBL; L26152; AAA26981.1; -
CC EMBL; L26153; AAA26982.1; -
CC EMBL; L26154; AAA26983.1; -
CC EMBL; L26155; AAA26984.1; -
CC EMBL; L26156; AAA26985.1; -
CC EMBL; L26157; AAA26986.1; -
CC EMBL; L26158; AAA26987.1; -
CC EMBL; L26159; AAA26988.1; -
CC EMBL; L26160; AAA26989.1; -
CC EMBL; L26161; AAA26990.1; -
CC EMBL; L26162; AAA26991.1; -
CC EMBL; AF104940; AAD17930.1; -
CC EMBL; AB030578; BAB16027.1; -

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OM protein - protein search, using sw model
Run on: September 17, 2005, 00:48:38 ; Search time 148.406 Seconds
(without alignments)
1614.846 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPQLHRSSLLVKNLQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1327.5	53.1	398	1	SPB STRPY	P00788 streptococ
2	1324.5	53.0	398	2	Q9AJD2	Q9ajd2 streptococ
3	1293.5	51.7	344	2	Q93LQ2	Q93lq2 streptococ
4	1130	45.2	251	2	Q8K6K5	Q8k6k5 streptococ
5	1129	45.2	251	1	SPB STRPY	P62561 streptococ
6	1129	45.2	251	1	SPB STRPY	P62560 streptococ
7	1096.5	43.9	236	2	Q54779	Q54779 streptococ
8	1095.5	43.8	222	2	Q98931	Q98931 streptococ
9	1095.5	43.8	236	2	P97163	P97163 streptococ
10	1089.5	43.6	236	2	Q57453	Q57453 streptococ
11	1027.5	41.1	220	2	Q79AQ0	Q79aq0 streptococ
12	986.5	39.5	236	2	Q54696	Q54696 streptococ
13	981.5	39.3	222	2	Q938P4	Q938p4 streptococ
14	981.5	39.3	222	2	Q985Z4	Q985z4 streptococ
15	541	21.6	266	1	ETXB STAAU	P01552 staphylococ
16	516	20.6	239	2	Q53678	Q53678 staphylococ
17	516	20.6	271	2	Q9F0L6	Q9f0l6 staphylococ
18	515	20.6	239	2	Q06532	Q06532 staphylococ
19	515	20.6	239	2	Q06533	Q06533 staphylococ
20	515	20.6	266	2	Q8NXJ6	Q8nxj6 staphylococ
21	513	20.5	239	2	Q05157	Q05157 staphylococ
22	513	20.5	239	2	Q06531	Q06531 staphylococ
23	513	20.5	266	1	ETC3 STAAU	P23313 staphylococ
24	510	20.4	239	2	Q06535	Q06535 staphylococ
25	510	20.4	239	2	Q6ST49	Q6st49 staphylococ
26	510	20.4	266	1	ETC2 STAAU	P34071 staphylococ
27	509	20.4	266	1	ETC1 STAAU	P01553 staphylococ
28	505	20.2	239	2	Q06534	Q06534 staphylococ
29	504	20.2	234	2	Q9R5X4	Q9r5x4 staphylococ
30	492.5	19.7	260	2	Q54971	Q54971 streptococ
31	487.5	19.5	260	2	Q54738	Q54738 streptococ

32	487.5	19.5	260	2	Q79X14	Q79x14 streptococ
33	487.5	19.5	260	2	Q54739	Q54739 streptococ
34	484	19.4	264	2	Q764P6	Q764p6 staphylococ
35	482	19.3	259	2	Q936G4	Q936g4 staphylococ
36	479	19.2	259	2	Q76LS8	Q76ls8 staphylococ
37	478.5	19.1	222	2	Q6XZE6	Q6xze6 staphylococ
38	475.5	19.0	222	2	Q6XZE7	Q6xze7 staphylococ
39	468	18.7	261	2	Q8XXM5	Q8xxm5 staphylococ
40	468	18.7	261	2	Q6YCN4	Q6ycn4 staphylococ
41	468	18.7	261	2	Q6GFN0	Q6gfn0 staphylococ
42	457	18.3	261	2	Q6XXM3	Q6xxm3 staphylococ
43	454	18.2	261	2	Q6XXM4	Q6xxm4 staphylococ
44	445.5	17.8	214	2	Q6XZE8	Q6xze8 staphylococ
45	444	17.8	233	2	Q8RR77	Q8rr77 staphylococ

ALIGNMENTS

RESULT 1
SPB STRPY STANDARD; PRT; 398 AA.
AC P00788; P26296; Q54960; Q54961; Q54962; Q54963; Q54964; Q54965;
AC Q54966; Q54967; Q54968; Q57024; Q57082; Q57202; Q57211; Q57212;
AC Q9S680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Streptopain precursor (SC 3.4.22.10) (Streptococcal cysteine
DE proteinase) (Streptococcus peptidase A) (SP) (Exotoxin type B) (SPE
DE B).
GN Name=speB;
GN OrderedLocNames=SPY2039, SPYM3_1742, SPS1739, SPYM18_2099;
OS Streptococcus pyogenes,
OS Streptococcus pyogenes (serotype M3), and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 198466, 186103;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-32 AND 146-162.
RC STRAIN=86-858, and NY-5;
RX MEDLINE=90330563; PubMed=2198264;
RA Hauser A.R., Schlievert P.M.;
RT "Nucleotide sequence of the streptococcal pyrogenic exotoxin type B
RT gene and relationship between the toxin and the streptococcal
RT proteinase precursor."
RL J. Bacteriol. 172:4536-4542 (1990).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=1226 / Serotype M44, 1233 / Serotype M17, 1251 / Serotype M3,
RC 1289 / Serotype M5, 1294 / Serotype M19, 156 / Serotype M18,
RC 157 / Serotype M3, 1590, 162 / Serotype M22, 165 / Serotype M,
RC 168 / Serotype M66, 1719 / Serotype T8, 1832 / Serotype M76,
RC 1838 / Serotype M27, 1841 / Serotype M41, 1842 / Serotype M43,
RC 1864 / Serotype M56, 1870, 1871, 1872, 1882 / Serotype M59, 1893,
RC 1896 / Serotype M10, 1898 / Serotype M15, 1901 / Serotype M23,
RC 1911 / Serotype M75, 1914A, 1990 / Serotype M, 1991 / Serotype M,
RC 2017 / Serotype M, 2018 / Serotype M, 262 / Serotype M,
RC 282 / Serotype M12, 289 / Serotype T28, 300 / Serotype M18,
RC 302 / Serotype M73, 303 / Serotype M6, 315 / Serotype M3,
RC 317 / Serotype M, 321 / Serotype M4, 327 / Serotype M2,
RC 366 / Serotype M30, 427 / Serotype M31, 429 / Serotype M8,
RC 587 / Serotype M28, 650 / Serotype M11, 659 / Serotype M13,
RC 660 / Serotype M14, 684 / Serotype M24, 686 / Serotype M25,
RC 719 / Serotype M49, 75 / Serotype M3, 758 / Serotype M75, and
RC 789 / Serotype M1, 796 / Serotype M9, 800 / Serotype M9, and
RC 807 / Serotype M33;
RX MEDLINE=94285789; PubMed=7516997; DOI=10.1006/mpat.1993.1083;
RA Kapur V., Topouzis S., Majesky M.W., Li L.L., Hamrick M.R.,
RA Hamill R.J., Patti J.M., Musser J.M.;
RT "A conserved Streptococcus pyogenes extracellular cysteine protease
RT cleaves human fibronectin and degrades vitronectin.";

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Query Match      20.4%; Score 509; DB 1; Length 266;
Best Local Similarity 44.7%; Pred. No. 7.5e-26;
Matches 105; Conservative 44; Mismatches 70; Indels 16; Gaps 6;

QY 2 QDDPSPQLHRSLSVKNL-QNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNVD 57
Db 30 QPDPTDELHKASKFTGLMENKVLVDYDHVVSATKSVKVDKFLADHLIYNISDKLKNVD 89

QY 58 KUKTELKQEMATLTKFKNKIDIVGEYHLCVCE-----NAERSACIGVTVNREGNH 110
Db 90 KVKTELLNEGLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGCKTGMCGITKEGHNH 149

QY 111 LEIP--KKIVVKVSDIGQSLFDETNNKMWTAQELDYKVRKYLTDNKLQNTGSPKYE 168
Db 150 FONGNLQNLVIRYENKRNITISFEVQTDKKSQVTAQELDIKARNFLINKNLKLYEFNSPYE 209

QY 169 TGVKIFIPKNKESFDFPFPEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGTWFYDMWPAQDFDQSKYLMYNDNKTVDKSKVIEVHLTTK 264

RESULT 12
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N3)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:O85382; GB:BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: seg
C:Superfamily: enterotoxin B

Query Match      17.8%; Score 444; DB 2; Length 258;
Best Local Similarity 43.3%; Pred. No. 1.2e-21;
Matches 101; Conservative 37; Mismatches 79; Indels 16; Gaps 6;

QY 2 QDDPSPQLHRSLSVKNL---LQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNVD 57
Db 26 QPDPKLDELNKVSDYKNNKGTMGVNVNLYTSPPEGRGVINSRQFLSHDLIFPIEYKSYN 85

QY 58 KUKTELKQEMATLTKFKNKIDIVGEYHLCVCE-----NAERSAC--IGVTVNREGNH 110
Db 86 EVKTELENTLANNYKDKVDIFGVFPYFTCTIPKSEPDINQFGCCMGGLTFNSSEN 145

QY 111 LEIPKKIVVKVSDIGQSLFDETNNKMWTAQELDYKVRKYLTDNKLQNTGSPKYEYTG 170
Db 146 -ERDKUITVQVITIDNRQSLGFTITNNKNWVTIQELDYKARHMLTEKKULYEDFGSAFEG 204

QY 171 YIKFIPKNKESFDFPFPEP---FTQSKYLMYKDNETLDSNT-QIEVILTT 219
Db 205 YIKFTEKNNTSFWDLFPKKELVPFPYKFLNLYGDNKVDKSKVIEVFLNT 257

RESULT 13
T10890
cysteine proteinase (EC 3.4.22.-) / hemagglutinin protein - Porphyromonas gingivalis
C:Species: Porphyromonas gingivalis
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10890
R:Madden, T.E.; Clark, V.L.; Kuramitsu, H.K.
Infect. Immun. 63, 238-247, 1995

A:Title: Revised sequence of the Porphyromonas gingivalis prtrr cysteine protease/hemaggl
A:Reference number: Z17199; MUID:95105001; PMID:7806362
A:Accession: T10890
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-886 <MAD>
A:Cross-references: UNIPROT:Q53481; EMBL:S75942; NID:g913136; PID:g913137
C:Genetics:
A:Gene: prtrr
C:Keywords: cysteine proteinase; hemagglutinin; hydrolase

Query Match      16.9%; Score 422; DB 2; Length 886;
Best Local Similarity 39.0%; Pred. No. 1.8e-19;
Matches 94; Conservative 37; Mismatches 94; Indels 16; Gaps 5;

QY 230 SKGIHYNQGNPNLLTPVIEKVPGEOSFVQCHAAATGCVATATQIMKYHNPYKGLKDY 289
Db 174 SDPLWDQGVFNTLHPLPS-----QQAYTGCVATAMGQIMRHYKWKPEKASGEY 224

QY 230 TYTSSNNPNYPNHPKNLFAAISTROYNNWNLPTYSGRESNVQKWAISELMADVGISYDM 349
Db 225 DYDDMTGTTH-THYSGTGF-----ETYNWSKMPGNISVGISPEVKALSTFVRDVSFSVNM 279

QY 350 DYGPSSGSAGSSRYORALKENFGYNOSVHOINRSDF-SODWEAQIDKELSONQPVYQGG 408
Db 280 QFADFGSGTTFIFVERALRETFHYKSLRYIHRLLPCKEWMIRKELAEINRPVYAGA 339

QY 409 KVG-CHAFVIDGAGRNPFHYNWGGVSDGFFRIDALNPALGTGGGAGFGNGVQSAVV 467
Db 340 DGSNGHAFVCDGYEPDGTGFHFHNGWGGMSGNGFYLNLLNLPGLSLGTGAGDGGYSTDQEVVI 399

QY 468 G 468
Db 400 G 400

RESULT 14
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match      12.1%; Score 303.5; DB 2; Length 136;
Best Local Similarity 47.4%; Pred. No. 6e-13;
Matches 64; Conservative 23; Mismatches 39; Indels 9; Gaps 3;

QY 95 ERSACIGVTVNREGNHL-----ETPKIVVKVSDIGQSLSFDETNNKMWTAQELDYK 148
Db 2 KKTCHYGVVTEHDGNDKNNSTDSNHLIKYENERNLSLFDIPTNNKNTAQEIDYK 61

QY 149 VRKYLTDNKLQNTGSPKYEYTKIFIPKNKESFDFPFPE--PEFTQSKYLMYKDNET 206
Db 62 VRNYLLKHKLNYEFNSPYETGYIKFIEGSHGSFYWDLMPESGKKFYPTKYLILLYNDNKT 121

QY 207 LDSNT-QIEVILTTK 220
Db 122 VESKSNVNEVHLTTK 136
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F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin B #status experimental <MAT>
F;120-140/Disulfide bonds: #status experimental

Query Match 21.6%; Score 541; DB 1; Length 266;
Best Local Similarity 47.7%; Pred. No. 6.3e-28;
Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNYD 57
Db 30 QPDPKPDDELHKSSEFTGTGNMKYLYDDHYVSATKVSVDKFLAHDLIYINSDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKKNIDYGVYHYLCLYCE-----NAERSACIGGVNREGNH 107
Db 90 NVRVFKNQDLADYKDKYVDFGVGANYIYOCYFSKKTNDINSHQTDKRTKCMYGVGTENH 149

QY 108 GNHLEIPKPKIVKVSIDGISOQLSFDIETNKKMVTQAELDYKVRKYLTDNKKQLYTNGPSKY 167
Db 150 GNQLDKYRSITVRVFDGKLLSFDVQTNKKVYTAQELDYLTRHYLVKKNKLYEFNNSPY 209

QY 168 ETGYIKFIPKNKESFWDFPFEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 221
Db 210 ETGYIKFIPKESFWDFPFEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 265

RESULT 9
S11885
enterotoxin C3 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S11885
R;Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
A;Reference number: S11885; MUID:90220508; PMID:2325627
A;Accession: S11885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <HOV>
A;Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C;Superfamily: enterotoxin B

Query Match 20.5%; Score 513; DB 2; Length 266;
Best Local Similarity 45.1%; Pred. No. 4.1e-26;
Matches 106; Conservative 43; Mismatches 70; Indels 16; Gaps 6;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNYD 57
Db 30 QPDPKPDDELHKSSEFTGTGNMKYLYDDHYVSATKVSVDKFLAHDLIYINSDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKKNIDYGVYHYLCLYCE-----NAERSACIGGVNREGNH 110
Db 90 KVKTLLNEDLAKKYKDEVDVYVGYNVCYFSSKDNVGVKVTGGKTCMYGGITKHEGHN 149

QY 111 LEIP--KKIVKVSIDGISOQLSFDIETNKKMVTQAELDYKVRKYLTDNKKQLYTNGPSKY 168
Db 150 FQNGNLQNLVRYENVKRNITISFEVQTDKSKVTAQELDIKARNFLINKNLYEFNNSPY 209

QY 169 TGYIKFIPKNKESFWDFPFEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGNTFWIDMMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVILTTK 264

RESULT 10
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N;Alternate names: enterotoxin C-3 precursor
C;Species: Staphylococcus aureus
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60114; B60114; A33866
R;Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A;Title: Conservation of the biologically active portions of staphylococcal enterotoxins

A;Reference number: A60114; MUID:89277549; PMID:2543637
A;Accession: A60114
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P34071
A;Accession: B60114
A;Molecule type: protein
A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests t
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 20.4%; Score 510; DB 2; Length 266;
Best Local Similarity 44.3%; Pred. No. 6.4e-26;
Matches 104; Conservative 45; Mismatches 70; Indels 16; Gaps 6;

QY 2 QQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSG---PNYD 57
Db 30 QPDPKPDDELHKSSEFTGTGNMKYLYDDHYVSATKVSVDKFLAHDLIYINSDKKLKNYD 89

QY 58 KLKTELKNQEMATLFDKKNIDYGVYHYLCLYCE-----NAERSACIGGVNREGNH 110
Db 90 KVKTLLNEDLAKKYKDEVDVYVGYNVCYFSSKDNVGVKVTGGKTCMYGGITKHEGHN 149

QY 111 LEIP--KKIVKVSIDGISOQLSFDIETNKKMVTQAELDYKVRKYLTDNKKQLYTNGPSKY 168
Db 150 FQNGNLQNLVRYENVKRNITISFEVQTDKSKVTAQELDIKARNFLINKNLYEFNNSPY 209

QY 169 TGYIKFIPKNKESFWDFPFEP--EFTQSKYLMYKDNETLDS-NTQIEVILTTK 220
Db 210 TGYIKFIENNGNTFWIDMMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVILTTK 264

RESULT 11
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness
A;Reference number: S06356; MUID:88038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R;Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
C;Genetics:
A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

QY 62 ELKNQEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIPIPKKIIVK 120
DB 83 ELKNQEMATLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIIVK 142
QY 121 VSDIGQSLSFDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFIPKNKE 180
DB 143 VSDIGQSLSFDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFIPKNKE 202
QY 181 SFWDFPPEFTQSKYLMYKDNETLDSNT 211
DB 203 SFWDFPPEFTQSKYLMYKDNETLDSNT 233
RESULT 6
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
N;Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S18789
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEL>
A:Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:947303; PIDN:CAA43771.1; PID:947304
A:Note: the nucleotide sequence was submitted to the EMBL data library, September 1991
C:Genetics:
A:Gene: speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>
Query Match 39.5%; Score 986.5; DB 2; Length 236;
Best Local Similarity 88.2%; Pred. No. 6.9e-57;
Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
QY 2 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 61
DB 23 QDDPNSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGLYNDKLT 82
QY 62 ELKNQEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIPIPKKIIVK 120
DB 83 ELKNREMTLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKNILVK 142
QY 121 VSDIGQSLSFDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFIPKNKE 180
DB 143 VSDIGQSLSFDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFISQKE 202
QY 181 SFWDFPPEFTQSKYLMYKDNETLDSNT 211
DB 203 TFWDFPPEFTQSKYLMYKDNETLDSNT 233
RESULT 7
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA

A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
Query Match 37.5%; Score 938.5; DB 1; Length 250;
Best Local Similarity 84.9%; Pred. No. 9.8e-54;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;
QY 5 PDPQSLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 64
DB 34 PKPSQLQRSNLVKTPEKIYFFMRVTLVTHENVKSVQDLRSHDLIYVSGPNYDKLKT 93
QY 65 NOEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIPIPKKIIVK 123
DB 94 NOEMATLFDKKNVDIIVSVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIIVK 153
QY 124 DGIQSLSPDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFIPKNKESFW 183
DB 154 DGIQSLSPDIETNKKMWTQAQLDYKVRKYLTNDKQLYTNGSPSKYETGYIKFIPKNKESFW 212
QY 184 FDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
DB 213 FDFPPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 250
RESULT 8
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029; PMID:3957869
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:Cross-references: UNIPROT:P01552; EMBL:M11118; NID:gi52999; PIDN:AAA88550.1; PID:gl530
A:Experimental source: strain S6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromid
A:Reference number: A92065; MUID:71007902; PMID:5470821
A:Accession: A92065
A:Molecule type: protein
A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',
A:Experimental source: strain S-6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositi
A:Reference number: A92064; MUID:71007901; PMID:5470820
A:Contents: annotation; chymotryptic peptides
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositi
A:Reference number: A92063; MUID:71007900; PMID:5470819
A:Contents: annotation; tryptic peptides
R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792; PMID:4953912
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Pogy, I.; Moskaleva, E.Y.; Sveshni
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A:Reference number: S27240; MUID:93049338; PMID:1425690
A:Accession: S27240
A:Molecule type: protein
A:Residues: 28-42; 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin

A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MGAS485 isolate California; strain MGAS251 isolate California; strain MGAS251 isolate United Kingdom; strain MGAS496 isolate Germany
 C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
 C;Accession: S18793; S18794; S18801; S18798
 R;Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A;Title: Characterization and clonal distribution of four alleles of the *speA* gene encoded by *Streptococcus pyogenes* strain MGAS158
 A;Reference number: S18782; MUID:92044323; PMID:1940804
 A;Accession: S18783
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61568; NID:G47289; PIDN:CAA43766.1; PID:G47290
 A;Experimental source: strain MGAS158 isolate Nebraska; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18793
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61569; NID:G47313; PIDN:CAA43767.1; PID:G47314
 A;Experimental source: strain MGAS485 isolate Yugoslavia; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18794
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61570; NID:G47315; PIDN:CAA43768.1; PID:G47316
 A;Experimental source: strain MGAS491 isolate United Kingdom; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18801
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61572; NID:G47333; PIDN:CAA43770.1; PID:G47334
 A;Experimental source: strain MGAS624 isolate Germany; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18798
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61571; NID:G47323; PIDN:CAA43769.1; PID:G47324
 A;Experimental source: strain MGAS495 isolate Germany; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C;Genetics:
 A;Gene: *speA3*
 C;Superfamily: enterotoxin B
 C;Keywords: exotoxin
 F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
 Query Match 43.9%; Score 1096.5; DB 2; Length 236;
 Best Local Similarity 98.6%; Pred. No. 5.1e-64;
 Matches 208; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
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 Db 23 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
 |||||
 QY 62 ELKNQEMATLFDKNDIYGVVEYHLCYLCENASACI-GGVTHREGNHLIPIPKIVVK 120
 |||||
 Db 83 ELKNQEMATLFDKNDIYGVVEYHLCYLCENASACIYGGVTHREGNHLIPIPKIVVK 142
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 QY 121 VSIDGIQSISFDIETNKKMVTQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
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 Db 143 VSIDGIQSISFDIETNKKMVTQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 202
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 QY 181 SFWFDFPPEFTQSKYLMYKDNETLDSNT 211
 |||||
 Db 203 SFWFDFPPEFTQSKYLMYKDNETLDSNT 233
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RESULT 5
 S18786
 exotoxin type A precursor (allele 2) - Streptococcus pyogenes phase (strain MGAS250 isolate)

N;Alternate names: scarlet fever toxin
 C;Species: Streptococcus pyogenes phase
 A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS251 isolate United Kingdom; strain MGAS496 isolate Germany
 C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
 C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
 R;Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A;Title: Characterization and clonal distribution of four alleles of the *speA* gene encoded by *Streptococcus pyogenes* strain MGAS250
 A;Reference number: S18782; MUID:92044323; PMID:1940804
 A;Accession: S18786
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61561; NID:G47297; PIDN:CAA43759.1; PID:G47298
 A;Experimental source: strain MGAS250 isolate California; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18787
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61562; NID:G47299; PIDN:CAA43760.1; PID:G47300
 A;Experimental source: strain MGAS251 isolate California; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18788
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61563; NID:G47301; PIDN:CAA43761.1; PID:G47302
 A;Experimental source: strain MGAS256 isolate California; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18790
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61564; NID:G47305; PIDN:CAA43762.1; PID:G47306
 A;Experimental source: strain MGAS285 isolate Colorado; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18792
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61565; NID:G47311; PIDN:CAA43763.1; PID:G47312
 A;Experimental source: strain MGAS480 isolate Yugoslavia; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18795
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61566; NID:G47317; PIDN:CAA43764.1; PID:G47318
 A;Experimental source: strain MGAS492 isolate United Kingdom; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18799
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NE>
 A;Cross-references: EMBL:X61567; NID:G47325; PIDN:CAA43765.1; PID:G47326
 A;Experimental source: strain MGAS496 isolate Germany; strain MGAS496 isolate Germany
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C;Genetics:
 A;Gene: *speA2*
 C;Superfamily: enterotoxin B
 C;Keywords: exotoxin
 F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
 Query Match 43.6%; Score 1089.5; DB 2; Length 236;
 Best Local Similarity 97.6%; Pred. No. 1.5e-63;
 Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
 |||||
 Db 23 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 82
 |||||

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 17, 2005, 01:00:14 ; Search time 33.847 Seconds
(without alignments)
1330.382 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: P1r1:.*
2: P1r2:.*
3: P1r3:.*
4: P1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	1327.5	53.1	398	2	A37768	streptococcal pyro	
2	1198	47.9	337	1	BP50P	streptopain (EC 3.	
3	1129	45.2	251	1	S29659	exotoxin type A pr	
4	1096.5	43.9	236	2	S18783	exotoxin type A pr	
5	1089.5	43.6	236	2	S18786	exotoxin type A pr	
6	986.5	39.5	236	2	S18789	exotoxin A precurs	
7	938.5	37.5	250	1	A26152	streptococcal pyro	
8	541	21.6	266	1	ENSAB6	enterotoxin B prec	
9	513	20.5	266	2	S11885	enterotoxin C3 - S	
10	510	20.4	266	2	A60114	enterotoxin C-2 pr	
11	509	20.4	266	1	ENSAC1	enterotoxin C-1 pr	
12	444	17.8	258	2	G89968	extracellular ente	
13	422	16.9	886	2	T10890	cysteine proteinase	
14	303.5	12.1	136	2	A89969	enterotoxin YENT2	
15	295.5	11.8	258	2	A33953	enterotoxin D prec	
16	291.5	11.7	260	2	B89969	enterotoxin SeO (i	
17	279.5	11.2	260	2	C89984	enterotoxin P (imp	
18	263	10.5	240	2	G89991	extracellular ente	
19	262.5	10.5	258	2	H89968	enterotoxin SeN (i	
20	257.5	10.3	257	2	A28664	enterotoxin A prec	
21	256.5	10.3	257	2	A28179	enterotoxin B prec	
22	237.5	9.5	239	2	D89969	enterotoxin SEM (i	
23	218	8.7	242	2	C89969	extracellular ente	
24	183	7.3	235	2	A30509	exotoxin C precurs	
25	173	6.9	133	2	B89969	enterotoxin Yent1	
26	154.5	6.2	825	2	H82885	hypothetical prote	
27	137	5.5	2500	2	G71609	hypothetical prote	
28	132.5	5.3	231	2	D89807	exotoxin 11 (impor	
29	124.5	5.0	750	2	G81361	probable flagellin	

30	124.5	5.0	1183	2	F90559	conserved hypothet
31	123.5	4.9	616	2	G82885	hypothetical prote
32	123	4.9	227	2	C89808	exotoxin 15 (impor
33	123	4.9	1215	2	B48281	cytotoxin-associat
34	122.5	4.9	960	2	S72284	DNA-directed RNA p
35	122.5	4.9	1146	2	A89922	conserved hypothet
36	121	4.8	1881	2	H95076	zinc metalloprotei
37	120.5	4.8	378	2	AD1541	hypothetical prote
38	120.5	4.8	2401	2	T28676	rhostry protein -
39	119	4.8	351	2	D89991	hypothetical prote
40	118	4.7	1306	2	T28313	ORF MSV152 probabl
41	117	4.7	675	2	S16624	penicillin-binding
42	117	4.7	1186	2	C64588	cag pathogenicity
43	116.5	4.7	770	2	B48910	desmocollin lb pre
44	116.5	4.7	824	2	A48910	desmocollin la pre
45	116.5	4.7	840	2	I37281	Dscia precursor -

ALIGNMENTS

RESULT 1

A37768
streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 22-Jun-1999
C:Accession: A37768
R:Hauser, A.R.; Schlievert, P.M.
J. Bacteriol. 172, 4536-4542, 1990
A:Title: Nucleotide sequence of the streptococcal pyrogenic exotoxin type B gene and re
A:Reference number: A37768; MUID:90330563; PMID:2198264
A:Accession: A37768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <HAU>
A:Cross-references: GB:M86905; GB:M35110; NID:g153818; PIDN:AAA26978.1; PID:g153819
C:Superfamily: streptococcal cysteine proteinase
C:Keywords: exotoxin

Query Match 53.1%; Score 1327.5; DB 2; Length 398;
Best Local Similarity 91.5%; Pred. No. 1.1e-78;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY	192	FTQSKYLMYKDNETHLSDNTQIEVYLT---	KQPVKSLSDSKGIHYNQNPYLLTPVI	248
Db	120	FMES-YVRQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGIHYNQNPYLLTPVI	173	
QY	249	EKKVPEGEOSFYGOHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYFNHPKQLFA	308	
Db	174	EKKVPEGEOSFYGOHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYFNHPKQLFA	233	
QY	309	AISTQYNNNLLPTYSRESNVQWALSELMDVIGISVDMYGFSSGSAGSSRVQALRK	368	
Db	234	AISTQYNNNLLPTYSRESNVQWALSELMDVIGISVDMYGFSSGSAGSSRVQALRK	293	
QY	369	ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYTG-KVKGGHAFVIDGADGRNFI	426	
Db	294	ENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYTGKVGKGGHAFVIDGADGRNFI	353	
QY	427	HYNWGCGVSDGFELDLNPSALGTGGAGGFGNGYQSAVVG	468	
Db	354	HYNWGCGVSDGFELDLNPSALGTGGAGGFGNGYQSAVVG	395	

RESULT 2

BP50P
streptopain (EC 3.4.22.10) precursor - Streptococcus pyogenes
N:Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A
C:Species: Streptococcus pyogenes
C>Date: 24-Apr-1984 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: S07668; A00978
R:Yonaha, K.; Elliott, S.D.; Liu, T.Y.
J. Protein Chem. 1, 317-334, 1982

RESULT 15

US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-308-830-13

Query Match 44.9%; Score 1122; DB 9; Length 251;
Best Local Similarity 97.3%; Pred. No. 1.2e-75;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

Qy 2 QDDPDPQLHRSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVSGPNYDKLKT 61
Db 31 QDDPDPQLHRSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVSGPNYDKLKT 90

Qy 62 ELKNQENATLFKKNIDIIYGVYTHLCYLCEAERSACI-GGVTNREGNHLEIPKKIIVK 120
Db 91 ELKNQENATLFKKNVDIYGVYTHLCYLCEAERSACIYGGVTNHEGHNLEIPKKIIVK 150

Qy 121 VSDIGIOSLFDIETNKKMTAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKPKNKE 180
Db 151 VSDIGIOSLFDIETNKKMTAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKPKNKE 210

Qy 181 SFWFDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTKK 220
Db 211 SFWFDFPPEFTQSKYLMYKDNETLDSNTQIEVYLTKK 251

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Job time : 146.152 secs

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; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/767,687
;   FILING DATE: 29-Jan-2004
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/882,431B
;   FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Charles H. Harris
;   REGISTRATION NUMBER: 34,616
;   REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 619-2065
;   TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 251
;     TYPE: Amino Acid
;     STRANDEDNESS: Unknown
;     TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

      Query Match      45.4%; Score 1136; DB 17; Length 251;
      Best Local Similarity 98.2%; Pred. No. 1.1e-76;
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QY      2 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db      31 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90

QY      62 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACI-GGVNREGNHLIPIPKIVVK 120
Db      91 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150

QY      121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db      151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 210

QY      181 SFWFDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db      211 SFWFDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 13
US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-163

      Query Match      45.2%; Score 1129; DB 16; Length 251;
      Best Local Similarity 97.7%; Pred. No. 3.7e-76;
      Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY      2 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db      31 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90

QY      62 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACI-GGVNREGNHLIPIPKIVVK 120
Db      91 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150

QY      121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db      151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 210

QY      181 SFWFDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db      211 SFWFDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 14
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

      Query Match      44.9%; Score 1122; DB 8; Length 251;
      Best Local Similarity 97.3%; Pred. No. 1.2e-75;
      Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY      2 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db      31 QQDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90

QY      62 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACI-GGVNREGNHLIPIPKIVVK 120
Db      91 ELKQEMATLFDKKNVDIYGYEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150

QY      121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db      151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 210

QY      181 SFWFDFPFPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db      211 SFWFDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251
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[illegible]

RESULT 10
US-08-882-431-16
Sequence 16, Application US/08882431
Publication No. US2003009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army NRMCC - 504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-16

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Db 151 VSIDIGISLFDIETNKKWVTAQELDYKVRKYLTDNKOLYTNGPSKYETGYIKFIPKNKE 210
Qy 181 SFWFDFPPEFTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWFDFPPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 11
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match 45.4%; Score 1136; DB 14; Length 251;
Best Local Similarity 98.2%; Pred. No. 1.le-76;
Matches 21; Conservative 1; Mismatches 1; Indels 2; Gaps 2

Qy 1 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
31 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
Db 62 ELKNQENMATLFDKKNVDIYGVEYHYLVCLENAERSACI-CGVTVREGNHLIEIPKIVVK 120
91 ELKNQENMATLFDKKNVDIYGVEYHYLVCLENAERSACIYGGVTNHEGNHLEIPKIVVK 150
Qy 121 VSIDIGISLFDIETNKKWVTAQELDYKVRKYLTDNKOLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSIDIGISLFDIETNKKWVTAQELDYKVRKYLTDNKOLYTNGPSKYETGYIKFIPKNKE 210
Qy 181 SFWFDFPPEFTQSKYLMYKONETLDSNT-QIEVYLTTK 220
Db 211 SFWFDFPPEFTQSKYLMYKONETLDSNTSQIEVYLTTK 251

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RESULT 12
US-10-767-687-16
Sequence 16, Application US/10767687
Publication NO. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Har
STREET: US Army MRCM -504
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

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RESULT 7
US-10-872-197A-25
; Sequence 25, Application US/10872197A
; Publication No. US20050059126A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOTSMIEIER
; APPLICANT: Ulrich KETTLING
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000203
; CURRENT APPLICATION NUMBER: US/10/872,197A
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-872-197A-25

Query Match          52.7%; Score 1316.5; DB 17; Length 371;
Best Local Similarity 91.1%; Pred. No. 6e-90;
Matches 257; Conservative 4; Mismatches 10; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHIHQGNPNYLLTPVI 248
Db 93 FMES-YVEQIKENKKLDS-----TYAGTAEIKQPVVKSLLDSKGHIHQGNPNYLLTPVI 146

QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 308
Db 147 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 206

QY 309 AISTQYNNNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVQRAK 368
Db 207 AISTQYNNNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVQRAK 266

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 426
Db 267 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 326

QY 427 HYNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
Db 327 HYNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 368

RESULT 8
US-11-021-951-25
; Sequence 25, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMIEIER, Christian
; APPLICANT: Ketting, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.000205
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-11-021-951-25

Query Match          52.7%; Score 1316.5; DB 20; Length 371;
Best Local Similarity 91.1%; Pred. No. 6e-90;
Matches 257; Conservative 4; Mismatches 10; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHIHQGNPNYLLTPVI 248
Db 93 FMES-YVEQIKENKKLDS-----TYAGTAEIKQPVVKSLLDSKGHIHQGNPNYLLTPVI 146

QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 308
Db 147 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 206

QY 309 AISTQYNNNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVQRAK 368
Db 207 AISTQYNNNNILPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVQRAK 266

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 426
Db 267 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFI 326

QY 427 HYNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
Db 327 HYNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 368

RESULT 9
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match          46.7%; Score 1168; DB 14; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.7e-79;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQDPPPSQLHRSSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNYSGPNYDKLK 60
Db 1 MQQDPPPSQLHRSSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNYSGPNYDKLK 60
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; SEQ ID NO 24
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin B prosegment
US-10-002-784A-24

Query Match          53.0%; Score 1324.5; DB 14; Length 398;
Best Local Similarity 71.7%; Pred. No. 1.7e-90;
Matches 273; Conservative 20; Mismatches 49; Indels 39; Gaps 10;

QY 95 ERSACI-GGVNREGNHLEPKKIVVKVSIIDGQSLSPDLETNK-KMVTAAQELDYKVKY 152
Db 47 QKSAALKAGARSADTKLD---KVLGGELSGSNMYGINISGGFVIVSGDKRRSPILGY 103

QY 153 LTDNKOLYTGPSKYETGIKFIKPKNESFWDFPEPEFTQSKYILMIYKDNETLDSNTQ 212
Db 104 STSG-----SFDANGKENI-----ASFMES-YVEQIKENKKLDT--- 136

QY 213 IEVYLTT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVIEKVKPGEQSFVGQHAATGCV 269
Db 137 --TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVIEKVKPGEQSFVGQHAATGCV 194

QY 270 TATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFAAISTROYNNNLLPTYSGRES 329
Db 195 TATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFAAISTROYNNNLLPTYSGRES 254

QY 330 NVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALKENFGYNQSVHQINRSDFS-QD 388
Db 255 NVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALKENFGYNQSVHQINRGDFSQD 314

QY 389 WEQAIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNFYHVNMGWGVSDGFFRLDALNP 447
Db 315 WEQAIDKELSONQPVYQOGVGKVGGHAFVIDGADGRNFYHVNMGWGVSDGFFRLDALNP 374

QY 448 SALGTGGGAGGNGYQSAVVG 468
Db 375 SALGTGGGAGGNGYQSAVVG 395

RESULT 5
US-10-474-792-642
; Sequence 642, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 642
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-642

Query Match          52.9%; Score 1323.5; DB 16; Length 398;
Best Local Similarity 91.1%; Pred. No. 2e-90;
Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
Db 120 FMES-YVEQIKENKKLDT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFA 308
Db 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFA 233
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QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALK 368
Db 234 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALK 293

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNFY 426
Db 294 ENFGYNQSVHQINRGDFSKQDWEAQIDKELSONQPVYQOGVGKVGGHAFVIDGADGRNFY 353

QY 427 HVNMGWGVSDGFFRLDALNPSALCTGGGAGGNGYQSAVVG 468
Db 354 HVNMGWGVSDGFFRLDALNPSALCTGGGAGGNGYQSAVVG 395

RESULT 6
US-10-872-198-25
; Sequence 25, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-872-198-25

Query Match          52.7%; Score 1316.5; DB 17; Length 371;
Best Local Similarity 91.1%; Pred. No. 6e-90;
Matches 257; Conservative 4; Mismatches 10; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLTT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
Db 93 FMES-YVEQIKENKKLDS-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 146

QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFA 308
Db 147 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPYKGLKDYTYTLSSNNPYENHPKNLFA 206

QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALK 368
Db 207 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGLISVDMYDGPSSGSAGSRVQRALK 266

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNFY 426
Db 267 ENFGYNQSVHQINRGDFSKQDWEAQIDKELSONQPVYQOGVGKVGGHAFVIDGADGRNFY 326

QY 427 HVNMGWGVSDGFFRLDALNPSALCTGGGAGGNGYQSAVVG 468
Db 327 HVNMGWGVSDGFFRLDALNPSALCTGGGAGGNGYQSAVVG 368
```


121 VSIDGQSLSDLETKKQWVTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
121 VSIDGQSLSDLETKKQWVTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
181 SFWDFPFPEFTQSKYLMYKDNETLDSNTQIEVYLTQKQPVVKSLLDSKGIHYNQGNP 240
181 SFWDFPFPEFTQSKYLMYKDNETLDSNTQIEVYLTQKQPVVKSLLDSKGIHYNQGNP 240
241 YNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
241 YNLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYF 300
301 NHPKNLFAAISTROYNNILPTYSGRESNVQMAISELMADVIGISVDMYDGPSSGSGS 360
301 NHPKNLFAAISTROYNNILPTYSGRESNVQMAISELMADVIGISVDMYDGPSSGSGS 360
361 SRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGVGGHAFVIDGA 420
361 SRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGVGGHAFVIDGA 420
421 DGRNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
421 DGRNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468

RESULT 2
US-10-002-784A-25
; Sequence 25, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 25
; TYPE: PRT
; LENGTH: 248
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B
US-10-002-784A-25

Query Match 53.3%; Score 1332; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.4e-91;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
221 QPVVKSLLDSKGIHYNQGNPNYLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYH 280
1 QPVVKSLLDSKGIHYNQGNPNYLLTPVIEKVRPGEOSFVGOHAATGCATATAQIMKYH 60
281 YPNKGLKDYTYTLSSNNPYFHPKNLFAAISTROYNNILPTYSGRESNVQMAISELM 340
61 YPNKGLKDYTYTLSSNNPYFHPKNLFAAISTROYNNILPTYSGRESNVQMAISELM 120
341 ADVGISVDMYDGPSSGSGSSRRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 400
121 ADVGISVDMYDGPSSGSGSSRRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 180
401 QPVYQGVGGHAFVIDGADGFNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFN 460
181 QPVYQGVGGHAFVIDGADGFNFYHVNWGVSDGFFRLDALNPSALGTGGGAGGFN 240
461 GYQSAVVG 468
241 GYQSAVVG 248

RESULT 3
US-10-428-817A-164
; Sequence 164, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-164

Query Match 53.1%; Score 1327.5; DB 16; Length 398;
Best Local Similarity 91.5%; Pred. No. 1e-90;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173
249 EKVPEGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYFHPKNLPA 308
174 EKVPEGEOSFVGOHAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYFHPKNLPA 233
309 AISTROYNNILPTYSGRESNVQMAISELMADVIGISVDMYDGPSSGSGSSRRVQRALK 368
234 AISTROYNNILPTYSGRESNVQMAISELMADVIGISVDMYDGPSSGSGSSRRVQRALK 293
369 ENFGYNQSVHQNRSDFS-QDWEAQIDKELSONQPVYQGVGGHAFVIDGADGFNFY 426
294 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGVGGHAFVIDGADGFNFY 353
427 HVNWGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
354 HVNWGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

RESULT 4
US-10-002-784A-24
; Sequence 24, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 17, 2005, 00:44:58 ; Search time 145.152 Seconds
(without alignments)
1305.574 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDDPPSQLHRSSLVKNLQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/us07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	468	14	US-10-002-784A-27
2	1332	53.3	248	14	US-10-002-784A-25
3	1327.5	53.1	398	16	US-10-428-817A-164
4	1324.5	53.0	398	14	US-10-002-784A-24
5	1323.5	52.9	398	16	US-10-474-792-642
6	1316.5	52.7	371	17	US-10-872-198-25
7	1316.5	52.7	371	17	US-10-872-197A-25
8	1316.5	52.7	371	20	US-11-021-951-25
9	1168	46.7	220	14	US-10-002-784A-26
10	1136	45.4	251	8	US-08-882-431-16
11	1136	45.4	251	14	US-10-002-784A-16

12	1136	45.4	251	17	US-10-767-687-16	Sequence 16, Appl
13	1129	45.2	251	16	US-10-428-817A-163	Sequence 163, App
14	1122	44.9	251	8	US-08-973-391A-13	Sequence 13, Appl
15	1122	44.9	251	9	US-09-308-830-13	Sequence 13, Appl
16	938.5	37.5	250	9	US-09-870-759-20	Sequence 20, Appl
17	938.5	37.5	250	10	US-09-751-708A-20	Sequence 20, Appl
18	938.5	37.5	250	16	US-10-428-817A-16	Sequence 16, Appl
19	938.5	37.5	250	17	US-10-937-758A-20	Sequence 20, Appl
20	543	21.7	239	9	US-09-150-947B-12	Sequence 12, Appl
21	543	21.7	239	14	US-10-172-425B-12	Sequence 12, Appl
22	541	21.6	238	16	US-10-428-817A-183	Sequence 183, Appl
23	541	21.6	255	15	US-10-354-948-2	Sequence 2, Appli
24	541	21.6	266	9	US-09-870-759-10	Sequence 10, Appl
25	541	21.6	266	10	US-09-751-708A-10	Sequence 10, Appl
26	541	21.6	266	16	US-10-428-817A-6	Sequence 6, Appli
27	541	21.6	266	17	US-10-937-758A-10	Sequence 10, Appl
28	539	21.6	266	14	US-10-151-336-8	Sequence 8, Appli
29	532	21.3	266	14	US-10-002-784A-6	Sequence 6, Appli
30	532	21.3	266	17	US-10-767-687-6	Sequence 6, Appli
31	530	21.2	239	14	US-10-002-784A-10	Sequence 10, Appl
32	530	21.2	239	17	US-10-767-687-10	Sequence 10, Appl
33	525	21.0	239	8	US-08-882-431-10	Sequence 10, Appl
34	523	20.9	266	14	US-10-002-784A-8	Sequence 8, Appli
35	523	20.9	266	17	US-10-767-687-8	Sequence 8, Appli
36	514	20.6	266	8	US-08-882-431-14	Sequence 14, Appl
37	514	20.6	266	14	US-10-002-784A-14	Sequence 14, Appl
38	514	20.6	266	17	US-10-767-687-14	Sequence 14, Appl
39	513.5	20.5	265	8	US-08-882-431-6	Sequence 6, Appli
40	513	20.5	240	17	US-10-923-324-4	Sequence 4, Appli
41	513	20.5	266	16	US-10-428-817A-186	Sequence 186, App
42	510	20.4	239	16	US-10-428-817A-185	Sequence 185, App
43	509	20.4	240	17	US-10-923-324-1	Sequence 1, Appli
44	509	20.4	266	9	US-09-870-759-12	Sequence 12, Appl
45	509	20.4	266	10	US-09-751-708A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27

Query Match	100.0%;	Score 2500;	DB 14;	Length 468;
Best Local Similarity	100.0%;	Pred. No. 2.8e-178;		
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLRSHDLIYNVSGPNYDKLK	60	
DB	1	MQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLRSHDLIYNVSGPNYDKLK	60	
QY	61	TELKQEMATLFDKKNIDIVGYEYHLVCYLCENASRSACIGGVTVNREGNHLIPKKIVVK	120	
DB	61	TELKQEMATLFDKKNIDIVGYEYHLVCYLCENASRSACIGGVTVNREGNHLIPKKIVVK	120	

Patent No. 6692746
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/09/708,008B
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US/08/896,933
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: 08/252,978
PRIOR FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match 37.5%; Score 938.5; DB 4; Length 220;
Best Local Similarity 84.9%; Pred. No. 5.5e-75;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;
QY 5 PDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLTELK 64
Db 4 PKPSQLQRNLVKTFKIYIFFMRVTLVTHENVKSVQDLRSHDLIYNVSGPNYDKLTELK 63
QY 65 NOEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIPKKIVVKVSI 123
Db 64 NOEMATLFDKKNIDIIYGVYHLCYLCEAERSACI-GGVTNREGNHLIPKKIVVKVSI 123
QY 124 DGQISLSDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKESFW 183
Db 124 DGQISLSDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKNKESFW 183
QY 184 DFFPEPFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 183 DFFPEPFTQSKYLMYKDNETLDSNTQIEVYLTK 220

Search completed: September 17, 2005, 00:48:31
Job time : 27.0362 secs

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 21.6%; Score 541; DB 1; Length 255;
Best Local Similarity 47.7%; Pred. No. 1.1e-39;
Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;
QY 2 QQDDPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGP---NYD 57
Db 19 QPDPKPDELHKSSKFTGLMNNMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYD 78
QY 58 KLKTELKNOEMATLFDKKNIDIIYGVYHLCYLCEA-----ERSACI-GGVTNRE 107
Db 79 NVRVFKNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINGSHQTDKRTKTCMYGGVTEHN 138
QY 108 GNHLEIPKKIVVKVSIIDGSIQSLSEFDIETNKKMVTAEQELDYKVRKYLTNDKQLYTNGPSKY 167
Db 139 GNQLDKYRSITVRVPEDEGKNLLSFDVQTNKKKVTAEQLDYLTRHYLVKRNKLYEFNNSPY 198
QY 168 ETGYIKFIPKNKESFWDFPEP--EFTQSKYLMYKDNETLDS-NTQIEVYLTKQ 221
Db 199 ETGYIKFI-ENENSFWYDMWMPAPGDKFDQSKYLMYNDNKKWYDVKDKVIEVYLTKK 254

Search completed: September 17, 2005, 00:48:31
Job time : 27.0362 secs

RESULT 15
US-08-446-918A-2
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

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Db 181 SFWDFPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 11
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoeck, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 44.9%; Score 1122; DB 4; Length 251;
Best Local Similarity 97.3%; Pred. No. 3.9e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QQDPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLTK 61
Db 31 QQDPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLTK 90
QY 62 ELKQEMATLFDKNDIYGYEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIIVK 120
Db 91 ELKQEMATLFDKNDIYGYEYHLCYLCEAERSACIYGGVTHNREGNHLIPIPKIIVK 150
QY 121 VSIDGQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 180
Db 151 VSIDGQSLSFDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPEFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 211 SFWDFPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 251

RESULT 12
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match 37.5%; Score 938.5; DB 3; Length 220;
Best Local Similarity 84.9%; Pred. No. 5.5e-75;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;

QY 5 PDPSSLHRSLSLVKLNQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLTK 64
Db 4 PKPSQLQRSNLVKTFKIYFFMRVTLVTHENVKSDQLRSHDLIYNVSGPNYDKLTK 63
QY 65 NOEMATLFDKNDIYGYEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIIVK 123
Db 64 NOEMATLFDKNDIYGYEYHLCYLCEAERSACIYGGVTHNREGNHLIPIPKIIVK 123
QY 124 DGIQSLSFEDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 183
Db 124 DGIQSLSFEDIETNKKMVTQAQELDYKVRKYLTDNKLTYNGSPSKYETGYIKFIPKNKE 182
QY 184 FDFPEFTQSKYLMYKDNETLDSNT-QIEVYLTK 220
Db 183 FDFPEFTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 14
US-09-708-008B-20
; Sequence 20, Application US/09708008B
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Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFPEPEFTQSKYLMYKONETLDSNTQIEVYLTK 221

RESULT 8

US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 44.9%; Score 1123; DB 3; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
QY 2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFPEPEFTQSKYLMYKONETLDSNTQIEVYLTK 221

RESULT 9

US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; EARLIER APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978

; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29

Query Match 44.9%; Score 1123; DB 4; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
QY 2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFPEPEFTQSKYLMYKONETLDSNTQIEVYLTK 221

RESULT 10

US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 44.9%; Score 1122; DB 4; Length 221;
Best Local Similarity 97.3%; Pred. No. 3.2e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
QY 2 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
Db 1 QODPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
QY 62 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLEIPKKIVVK 120
Db 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120
QY 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPEPEFTQSKYLMYKONETLDSNT-QIEVYLTK 220
Db 181 SFWDFPEPEFTQSKYLMYKONETLDSNTQIEVYLTK 221

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; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

Query Match 45.4%; Score 1136; DB 3; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.2e-92;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 61
Db 31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db 91 ELKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLIPIPKIVVK 150
QY 121 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSIEVYLTTK 251

RESULT 6
US-08-882-431B-16
; Sequence 16, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

Query Match 45.4%; Score 1136; DB 3; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.2e-92;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 61
Db 31 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db 91 ELKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLIPIPKIVVK 150
QY 121 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 210
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT-QIEVYLTTK 220
Db 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSIEVYLTTK 251

RESULT 7
US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match 44.9%; Score 1123; DB 3; Length 221;
Best Local Similarity 97.3%; Pred. No. 2.6e-91;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 61
Db 1 QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 60
QY 62 ELKQEMATLFDKKNIDYGVVEYHLCYLCEAERSACI-GGVTNREGNHLIPIPKIVVK 120
Db 61 ELKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGHNHLIPIPKIVVK 120
QY 121 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 180
Db 151 VSDIGIQSLSFDIETNKKMVTQAQELDYKVRKYLTNKKQLYTNGPSKYETGYIKFIPKNKE 210
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```

; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.
; AUTHORS: Hamrick, M. R.
; AUTHORS: Hamill, R. J.
; AUTHORS: Patti, J. M.
; AUTHORS: Musser, J. M.
; TITLE: A conserved Streptococcus pyogenes
; TITLE: extracellular cysteine protease cleaves human
; TITLE: fibronectin and degrades vitronectin
; JOURNAL: Microb. Pathog.
; VOLUME: 15
; PAGES: 327-346
; DATE: 1993
; US-08-931-220-5

Query Match      53.1%; Score 1327.5; DB 3; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDLT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLFA 308
DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLFA 233

QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMVDPSSGSGSSRVQRAALK 368
DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMVDPSSGSGSSRVQRAALK 293

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNPFY 426
DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKVGKGFHAFVIDGADGRNPFY 353

QY 427 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

RESULT 3
PCT-US95-11723-5
; Sequence 5, Application PC/TUS9511723
; GENERAL INFORMATION:
; APPLICANT: Musser M.D., James M.
; APPLICANT: Kapur M.D., Vivek
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Identifying Streptococcus
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAW OFFICES OF BARBARA RAE-VENTER
; STREET: P.O. Box 60039
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,542
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter Ph.D., Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: BAYL-004/03US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6205
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes
; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.

; STRAIN: MGAS 1719
; IMMEDIATE SOURCE:
; CLONE: SPEB7 (cysteine protease)
; PUBLICATION INFORMATION:
; AUTHORS: Kapur, V.
; AUTHORS: Topouzis, S.
; AUTHORS: Majesky, M. W.
; AUTHORS: Li, L.-L.
; AUTHORS: Hamrick, M. R.
; AUTHORS: Hamill, R. J.
; AUTHORS: Patti, J. M.
; AUTHORS: Musser, J. M.
; TITLE: A conserved Streptococcus pyogenes
; TITLE: extracellular cysteine protease cleaves human
; TITLE: fibronectin and degrades vitronectin
; JOURNAL: Microb. Pathog.
; VOLUME: 15
; PAGES: 327-346
; DATE: 1993
; US-10-030-330-6

Query Match      53.1%; Score 1327.5; DB 4; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDLT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

QY 249 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLFA 308
DB 174 EKVKPGEQSFVGOHAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYFNHPKNLFA 233

QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMVDPSSGSGSSRVQRAALK 368
DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVIGISVDMVDPSSGSGSSRVQRAALK 293

QY 369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSONQPVYQOG-GKVGGHAFVIDGADGRNPFY 426
DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKVGKGFHAFVIDGADGRNPFY 353

QY 427 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HVNWGMGGVSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

RESULT 2
US-10-030-330-6
; Sequence 6, Application US/10030330
; Patent No. 6833262
; GENERAL INFORMATION:
; APPLICANT: The University of Georgia Research Foundation, Inc
; TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
; FILE REFERENCE: 235.00210201
; CURRENT APPLICATION NUMBER: US/10/030,330
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/130,436
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-10-030-330-6

Query Match      53.1%; Score 1327.5; DB 4; Length 398;
Best Local Similarity 91.5%; Pred. No. 5.1e-109;
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDLT-----TYAGTAETIKQPVVKSLLDSKGIHYNQGNPNYLLTPVI 173

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 00:42:17 ; Search time 26.0362 Seconds
(without alignments)
1341.817 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MQQDPDPSQLHRSLSLVKNLQ.....ALCTGGAGGFNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCUTS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	1327.5	53.1	398	3	US-08-931-220-5
2	1327.5	53.1	398	4	US-10-030-330-6
3	1327.5	53.1	398	5	PCT-US95-11723-5
4	1327.5	53.1	398	5	PCT-US96-05997-1
5	1136	45.4	251	3	US-09-144-776B-16
6	1136	45.4	251	4	US-08-882-431B-16
7	1123	44.9	221	3	US-08-896-933-29
8	1123	44.9	221	3	US-09-314-235-29
9	1123	44.9	221	4	US-09-708-008B-29
10	1122	44.9	221	4	US-08-973-391C-14
11	1122	44.9	221	4	US-08-973-391C-13
12	938.5	37.5	220	3	US-08-896-933-20
13	938.5	37.5	220	3	US-09-314-235-20
14	938.5	37.5	220	4	US-09-708-008B-20
15	541	21.6	255	1	US-08-446-918A-2
16	541	21.6	255	2	US-08-580-806-2
17	539	21.6	266	3	US-09-414-276-8
18	532	21.3	266	3	US-09-144-776B-6
19	532	21.3	266	4	US-08-882-431B-6
20	530	21.2	239	3	US-09-144-776B-10
21	530	21.2	239	4	US-08-882-431B-10
22	528	21.1	239	3	US-08-896-933-26
23	528	21.1	239	3	US-09-314-235-26
24	528	21.1	239	4	US-09-708-008B-26
25	523	20.9	266	3	US-09-144-776B-8
26	523	20.9	266	4	US-08-882-431B-8
27	514	20.6	266	3	US-09-144-776B-14

28	514	20.6	266	4	US-08-882-431B-14	Sequence 14, Appl
29	510	20.4	238	3	US-08-896-933-28	Sequence 28, Appl
30	510	20.4	238	3	US-09-314-235-28	Sequence 28, Appl
31	510	20.4	238	4	US-09-708-008B-28	Sequence 28, Appl
32	509	20.4	239	3	US-08-896-933-27	Sequence 27, Appl
33	509	20.4	239	3	US-09-314-235-27	Sequence 27, Appl
34	509	20.4	239	4	US-09-708-008B-27	Sequence 27, Appl
35	489	19.6	239	3	US-08-896-933-21	Sequence 21, Appl
36	489	19.6	239	3	US-09-314-235-21	Sequence 21, Appl
37	489	19.6	239	4	US-09-708-008B-21	Sequence 21, Appl
38	414	16.6	840	4	US-10-030-330-5	Sequence 5, Appl
39	397.5	15.9	79	3	US-09-144-776B-24	Sequence 24, Appl
40	397.5	15.9	79	4	US-08-882-431B-24	Sequence 24, Appl
41	393	15.7	843	4	US-10-030-330-1	Sequence 1, Appl
42	295.5	11.8	228	3	US-08-896-933-25	Sequence 25, Appl
43	295.5	11.8	228	3	US-09-314-235-25	Sequence 25, Appl
44	295.5	11.8	228	4	US-09-708-008B-25	Sequence 25, Appl
45	257.5	10.3	233	1	US-08-446-918A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-931-220-5
; Sequence 5, Application US/08931220
; Patent No. 6030835
; GENERAL INFORMATION:
; APPLICANT: Musser M.D., James M.
; APPLICANT: Kapur M.D., Vivek
; TITLE OF INVENTION: Methods and Compositions for Identifying
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 2882 Sand Hill Road, Suite 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025-7022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,220
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,542
; FILING DATE: 14-SEP-1994
; APPLICATION NUMBER: US 08/160,965
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter Ph.D., Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: BAYL-004/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pyogenes

PF 20-APR-2000; 2000WO-US010574.
XX
XX 21-APR-1999; 99US-0130436P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (TRAV/) TRAVIS J.
PA (POTE/) POTEMPA J.
PA (NELS/) NELSON D.
XX
PI Travis J, Potempa J, Nelson D;
XX
XX WPI; 2000-679600/66.
XX
XX Novel oral bacterial periodontain polypeptide for treating periodontal
PT diseases, has amidolytic activity for cleavage of non-denatured human
PT alphas-proteinase inhibitor at reactive site loop region of inhibitor.
XX
XX Example 1; Fig 1; 55pp; English.
XX
XX The present sequence is given in a specification relating to novel oral
CC bacterial polypeptide referred to as periodontain. The polypeptide has
CC amidolytic activity for cleavage of denatured polypeptides and non-
CC denatured serpin polypeptides. It has amidolytic activity for cleavage of
CC a non-denatured human alpha 1-proteinase inhibitor at a reactive site
CC loop region of the inhibitor. Periodontain is useful for inhibiting the
CC peptidase activity and reducing periodontitis, loss of tooth attachment
CC and periodontal pocket formation, and for reducing growth of bacteria,
CC preferably P. gingivalis in vitro or in vivo. It is useful for protecting
CC an animal from a disease caused by P. gingivalis and for treating
CC periodontal diseases, including gingivitis and periodontitis
XX
XX Sequence 398 AA;
Query Match 47.8%; Score 1195.5; DB 3; Length 398;
Best Local Similarity 84.0%; Pred. No. 1.3e-88;
Matches 237; Conservative 5; Mismatches 29; Indels 11; Gaps 5;
QY 192 FTQSKYLMYIKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNYLLTPVI 248
DB 120 FMES-YVEQIKENKLDI-----TYAGTAIEIKQPVKSLDSKGIHYNQGNPNYLLTPXX 173
QY 249 EKVKGESQSFVGQHAATGCVATATAQIMKYHYNPNKGLKDYTYTLSSNNPYFNHPKNLFA 308
DB 174 EKVKGESQSFVGQHAATGCVATATAQIMKYHKNPNKGLKXXYTYTLSSNNPYFNHPKNLXX 233
QY 309 AISTROYNNILPTYSGRESNVQKMAISELMADVIGISVDMYDYGPSGSGSAGSRVORALX 368
DB 234 XISTROYNNILPTYSGRESNVQKMAISELMADVIGISVDMYDYGPSGSGSAGSRVORALX 293
QY 369 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFX 426
DB 294 ENFGYNQSVHQNRSDFSQDWEAQIDKELSONQPVYQGG-KVGGHAFVIDGADGRNFX 353
QY 427 HYNMGWGGYSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 468
DB 354 HYNMGWGGYSDGFFRLDALNPSALGTGGGAGGNGYQSAVVG 395

Search completed: September 17, 2005, 01:09:43
Job time : 154.962 secs

CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX Sequence 398 AA;

Query Match 52.9%; Score 1323.5; DB 5; Length 398;
 Best Local Similarity 91.1%; Pred. No. 4.6e-99;
 Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHYNQGNPNYLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGHYNQGNPNYLLTPVI 173
 QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYNFHPKNLFA 308
 DB 174 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYNFHPKNLFA 233
 QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 368
 DB 234 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 293
 QY 369 ENFGYNQSVHQINRDFSKQDWEAQIDKELSONQPVYQGG-KGVGGHAFVIDGADGRNFI 426
 DB 294 ENFGYNQSVHQINRDFSKQDWEAQIDKELSONQPVYQGG-KGVGGHAFVIDGADGRNFI 353
 QY 427 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 DB 354 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 12

AAE37685
 ID AAE37685 standard; protein; 398 AA.

AC AAE37685;

XX 06-OCT-2003 (first entry)

XX Streptococcus pyogenes pyrogenic exotoxin B (SpeB) protein.

XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
 XX gene therapy.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers

FT Peptide

FT 1..145 /label= Signal_peptide

FT Protein

FT 146..398 /note= "S. pyogenes mature SpeB protein"

XX WO2003056015-A1.

XX 10-JUL-2003.

XX 26-NOV-2001; 2001WO-US046540.

XX 26-NOV-2001; 2001US-00002784.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

PI Ulrich RG;

XX WPI; 2003-492125/46.

XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.

XX Example 14; Page 133; 141pp; English.

XX The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is Streptococcus pyogenes
 CC pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
 CC invention

XX Sequence 398 AA;

Query Match 52.9%; Score 1323.5; DB 7; Length 398;
 Best Local Similarity 91.1%; Pred. No. 4.6e-99;
 Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVYLT---KQPVVKSLLDSKGHYNQGNPNYLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAETKQPVVKSLLDSKGHYNQGNPNYLLTPVI 173
 QY 249 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYNFHPKNLFA 308
 DB 174 EKVKPEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYNFHPKNLFA 233
 QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 368
 DB 234 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSSRVORALK 293
 QY 369 ENFGYNQSVHQINRDFSKQDWEAQIDKELSONQPVYQGG-KGVGGHAFVIDGADGRNFI 426
 DB 294 ENFGYNQSVHQINRDFSKQDWEAQIDKELSONQPVYQGG-KGVGGHAFVIDGADGRNFI 353
 QY 427 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 468
 DB 354 HVNMGWGGVSDGFFRLDALNPSALGTGGGAGGFGNGYQSAVVG 395

RESULT 13

ADR83971

ID ADR83971 standard; protein; 398 AA.

XX ADR83971;

AC ADR83971;

XX 02-DEC-2004 (first entry)

XX S. pyogenes hyperimmune system reactive antigen Spy2039.

XX hyperimmune serum reactive antigen; vaccine; anticaline.

XX Streptococcus pyogenes.

XX WO2004078907-A2.

XX 16-SEP-2004.

XX 02-MAR-2004; 2004WO-EP002087.

XX 04-MAR-2003; 2003EP-00450061.

XX (INTE-) INTERCELL AG.

XX Meinke A, Nagy E, Winkler B, Gelbmann D;

XX WPI; 2004-653698/63.

XX N-PSDB; ADR83821.

XX OS Streptococcus pyogenes.
 XX PN US6030835-A.
 XX PD 29-FEB-2000.
 XX PF 16-SEP-1997; 97US-00931220.
 XX PR 02-DEC-1993; 93US-00160965.
 XX PR 14-SEP-1994; 94US-00306542.
 XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX PI Kapur V, Musser JM;
 XX DR WPI; 2000-205208/18.
 XX DR N-PSDB; AAA07111.
 XX PT Determining the presence of a Group A Streptococcus expressing a protease
 PT capable of degrading proteins of the extracellular matrix, using a
 PT specific antibody.
 XX PS Disclosure; Col 7-8; 56pp; English.
 XX CC This sequence represents the S. pyogenes cysteine protease speB7. The
 CC invention relates to a method for determining the presence of a Group A
 CC Streptococcus which expresses an extracellular protease (preferably speB)
 CC capable of degrading proteins of the extracellular matrix, comprising:
 CC (1) combining a sample with an assay medium comprising a first member of
 CC a specific binding pair which binds to a second member of the binding
 CC pair to form a complex, where the first member has at least 1 epitopic
 CC site competitive with at least 1 conserved epitopic site on the protease;
 CC and (2) detecting complex formation as indicative of the presence of the
 CC pathogenic organism. The method is useful for screening host samples for
 CC evidence of infection with Streptococcus pyogenes and for monitoring the
 CC disease status of the host. The speB gene products are used as a vaccine
 CC for protecting against Streptococcus mediated diseases such as
 CC pharyngitis, tonsillitis, skin infections, scarlet fever, sepsis,
 CC erysipelas, fasciitis, pneumonia, acute rheumatic fever,
 CC poststreptococcal glomerulonephritis, cellulitis, bacteraemia, and
 CC meningitis
 XX SQ Sequence 398 AA;
 Query Match 53.1%; Score 1327.5; DB 3; Length 398;
 Best Local Similarity 91.5%; Pred. No. 2.2e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIIHYNGNPYNLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIIHYNGNPYNLLTPVI 173
 QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 308
 DB 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 233
 QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMVDPGSSGSGSRRVQALK 368
 DB 234 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMVDPGSSGSGSRRVQALK 293
 QY 369 ENFGYNQSVHQINRSDFS-ODWEAQIDKELSONQPVYQOG-GKVGGHAFVIGADGRNFY 426
 DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVGVGVGHAFVIGADGRNFY 353
 QY 427 HVNMGVGGVSDGFFRLDALNPSALGTGGGAGGFGNGQSAVVG 468
 DB 354 HVNMGVGGVSDGFFRLDALNPSALGTGGGAGGFGNGQSAVVG 395
 RESULT 9
 ADF89840
 ID ADF89840 standard; protein; 398 AA.

XX ADF89840;
 XX AC 26-FEB-2004 (first entry)
 XX DT Streptococcal pyrogenic exotoxin B (SpEB) sequence..
 XX DE Superantigen; SAg; enterotoxin; cytostatic; gene therapy; cancer;
 XX KW pyrogenic exotoxin; SpE; SpEB.
 XX OS Streptococcus sp.
 XX PN WO2003094846-A2.
 XX PD 20-NOV-2003.
 XX PF 08-MAY-2003; 2003WO-US014381.
 XX PR 08-MAY-2002; 2002US-0378988P.
 XX PR 15-JUN-2002; 2002US-0389366P.
 XX PR 28-AUG-2002; 2002US-0406697P.
 XX PR 29-AUG-2002; 2002US-0406750P.
 XX PR 01-OCT-2002; 2002US-0415310P.
 XX PR 02-OCT-2002; 2002US-0415400P.
 XX PR 09-JAN-2003; 2003US-0438686P.
 XX (TERM/) Terman D S.
 XX PA Terman DS;
 XX PI WPI; 2004-011997/01.
 XX DR Treating a subject with cancer or malignant diseases comprises
 PT intratumoral, intrathecal or intracavitary administration of an amount of
 PT a superantigen composition to the subject.
 XX PS Disclosure; SEQ ID NO 17; 91pp; English.
 XX CC The invention relates to treating a subject with cancer. The method
 CC involves administering an amount of a superantigen (SAG) composition
 CC comprising a molecule selected from: a native SAG protein; its
 CC biologically active fragment or a biologically active homologue or a
 CC biologically active fusion protein comprising the SAG or its fragment or
 CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
 CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
 CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and
 CC Clostridium perfringens exotoxin. The method is useful in treating cancer
 CC or malignant diseases such as malignant pleural effusion, ascites,
 CC pericardial effusion or meningeal carcinomatosis. The present sequence
 CC represents a Streptococcal pyrogenic exotoxin B (SpEB).
 XX SQ Sequence 398 AA;
 Query Match 53.1%; Score 1327.5; DB 8; Length 398;
 Best Local Similarity 91.5%; Pred. No. 2.2e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIIHYNGNPYNLLTPVI 248
 DB 120 FMES-YVEQIKENKKLDT-----TYAGTAIEIKQPVVKSLLDSKGIIHYNGNPYNLLTPVI 173
 QY 249 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 308
 DB 174 EKVKPGEQSFVGQHAATGCVATATAQIMKYHNPKNGLKDYTYTLSSNNPYFNHPKNLFA 233
 QY 309 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMVDPGSSGSGSRRVQALK 368
 DB 234 AISTROYNNNLLPTYSGRESNVQKMAISELMADVGISVDMVDPGSSGSGSRRVQALK 293
 QY 369 ENFGYNQSVHQINRSDFS-ODWEAQIDKELSONQPVYQOG-GKVGGHAFVIGADGRNFY 426
 DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVGVGVGHAFVIGADGRNFY 353

XX The present sequence is the Streptococcus pyogenes clone speB7 pre-pro
 CC cysteine protease (CP), which can be used to inhibit neoplastic cell
 CC proliferation, especially in a human, useful in the treatment of
 CC neoplastic conditions, e.g. carcinomas, sarcomas, melanomas, lymphomas
 CC and leukemias originating from blood, lung, mammary gland, prostate,
 CC intestine, stomach, liver, heart, skin, pancreas or brain tissue. The CP
 CC is especially associated with a wound covering, and can also be used to
 CC prevent metastasis or identify susceptible neoplastic cells. K1735 and
 CC CM519 melanoma cells were injected s.c. into nu/nu mice, optionally
 CC followed by i.p. injection of CP (100 microg, 24 hours later). The mice
 CC were checked twice weekly for tumour growth for 12 weeks, to give results
 CC that showed that treatment with CP completely protected athymic mice
 CC against transplanted K1735 melanoma growth, and protected 60% of the mice
 CC from developing CM519 melanomas

XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 2; Length 398;
 Best Local Similarity 91.5%; Pred. No. 2.2e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248
 DB 120 FMES-YVEQIKENKLDLT-----TYAGTAIEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173
 QY 249 EKVKPGEQSFVQGHAAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 308
 DB 174 EKVKPGEQSFVQGHAAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 233
 QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRSRVORALK 368
 DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRSRVORALK 293
 QY 369 ENFGYNQSVHQINRSDFS-ODWEAQIDKELSONQPVYQOG-GKVGGHAFVIGADGRNFY 426
 DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKGVGGHAFVIGADGRNFY 353
 QY 427 HVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468
 DB 354 HVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

RESULT 7

AAR95856
 ID AAR95856 standard; protein; 398 AA.

XX AC AAR95856;

XX DT 30-OCT-1996 (first entry)

XX DE S. pyogenes speB gene encoded extracellular protease.

XX Immunogenic peptide; speB gene; extracellular protease; production;
 KW antibody; vaccine; diagnosis; detection; Streptococcus infection;
 KW group A; prevention; treatment; pharyngitis; tonsillitis; skin infection;
 KW acute rheumatic fever; scarlet fever; probe;
 KW post-streptococcal glomerulonephritis; sepsis; meningitis; erysipellis;
 KW cellulitis; fasciitis; toxic shock like syndrome.

XX OS Streptococcus pyogenes.

XX FH Key Location/Qualifiers
 FT Misc-difference 216

FT /note= "corresponding codon TAG"

FT Domain 333..338

FT /label= putative nucleotide binding domain

FT Region 382..398

FT /label= potential collagen docking region

XX WO9608569-A2.

XX PN post-streptococcal glomerulonephritis; sepsis; meningitis; erysipellis;
 XX KW cellulitis; bacteremia; meningitis.

PD 21-MAR-1996.

XX

PF 13-SEP-1995; 95WO-US011723.

XX 14-SEP-1994; 94US-00306542.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Musser JA, Kapur V;

XX WPI; 1996-179944/18.

XX DR N-PSDB; AAT15294.

XX Use of extracellular protease(s), partic. cysteine protease - for

PT detection, diagnosis prevention and treatment of infection by pathogenic

PT organisms, partic. gp. A streptococcus strains.

XX Disclosure; Page 12; 97pp; English.

XX The present sequence is the S. pyogenes speB gene encoded extracellular

CC protease. An immunogenic peptide derived from the protease can be used in

CC the prodn. of antibody (Ab) and vaccine. Ab is prepd. by introducing the

CC peptide into a mammal, pref. a mouse, followed by Ab isolation. The Ab or

CC a probe derived from the gene can be used for the diagnosis and detection

CC of gp. A Streptococcus infections, while vaccine, which inhibits

CC streptococcal replication, can be used to prevent and treat gp. A

CC Streptococcus infections, and partic. to ameliorate pharyngitis,

CC tonsillitis, skin infections, acute rheumatic fever, scarlet fever, post-

CC streptococcal glomerulonephritis, sepsis, meningitis, erysipellis,

CC cellulitis, fasciitis and toxic shock like syndrome

XX SQ Sequence 398 AA;

Query Match 53.1%; Score 1327.5; DB 2; Length 398;

Best Local Similarity 91.5%; Pred. No. 2.2e-99;

Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

QY 192 FTQSKYLMYKDNETLDSNTQIEVLT---KQPVVKSLLDSKGIHYNQGNPNLLTPVI 248

DB 120 FMES-YVEQIKENKLDLT-----TYAGTAIEIKQPVVKSLLDSKGIHYNQGNPNLLTPVI 173

QY 249 EKVKPGEQSFVQGHAAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 308

DB 174 EKVKPGEQSFVQGHAAATGCATATAQIMKYHNPKNGLKDYTYTLSSNNPYNFHPKNLFA 233

QY 309 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRSRVORALK 368

DB 234 AISTROYNNWNLPTYSGRESNVQKMAISELMADVGISVDMYDGPSSGSGSRSRVORALK 293

QY 369 ENFGYNQSVHQINRSDFS-ODWEAQIDKELSONQPVYQOG-GKVGGHAFVIGADGRNFY 426

DB 294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSONQPVYQOGVKGVGGHAFVIGADGRNFY 353

QY 427 HVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 468

DB 354 HVNWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVG 395

RESULT 8

AAY81812

ID AAY81812 standard; protein; 398 AA.

XX AC AAY81812;

XX DT 09-JUN-2000 (first entry)

XX S. pyogenes cysteine protease speB7 protein sequence.

XX Cysteine protease; speB; Group A Streptococcus; extracellular protease;

KW detection; diagnosis; extracellular matrix; infection; skin infection;

KW disease status monitoring; vaccine; Streptococcus mediated disease;

KW pharyngitis; tonsillitis; scarlet fever; sepsis; erysipellis; fasciitis;

KW pneumonia; acute rheumatic fever; poststreptococcal glomerulonephritis;

KW cellulitis; bacteremia; meningitis.

CC SPEB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the wild-type SPEB mature protein

XX SQ Sequence 248 AA;
Query Match 53.3%; Score 1332; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 4.7e-100;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 280
Db 1 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 60
QY 281 YPNKGLKDYTYTLSSNNPFNFHPKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 340
Db 61 YPNKGLKDYTYTLSSNNPFNFHPKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 120
QY 341 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 400
Db 121 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 180
QY 401 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
Db 181 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 240
QY 461 GYQSAVVG 468
Db 241 GYQSAVVG 248

RESULT 5
AAE37686
ID AAE37686 standard; protein; 248 AA.
XX AC AAE37686;
XX DT 06-OCT-2003 (first entry)
XX DE Streptococcus pyogenes mature pyrogenic exotoxin B (SpeB) protein.
XX KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin B; SpeB;
XX KW Gene therapy.
XX OS Streptococcus pyogenes.
XX PN WO2003056015-A1.
XX PD 10-JUL-2003.
XX PF 26-NOV-2001; 2001WO-US046540.
XX PR 26-NOV-2001; 2001US-00002784.
XX (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PA Ulrich RG;
XX PI WPI; 2003-492125/46.
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.
XX PS Example 14; Page 134; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
CC genetically altered such that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is disrupted or
CC altered. DNA fragments of the invention are useful in the production of
CC vaccines against bacterial superantigen toxin infections. They are also
CC useful in gene therapy. The present sequence is Streptococcus pyogenes
CC mature pyrogenic exotoxin B (SpeB) protein. This sequence is used in the
CC invention

XX SQ Sequence 248 AA;
Query Match 53.3%; Score 1332; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 4.7e-100;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 221 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 280
Db 1 QPVVKSLLDSKGIHYNQGNPNLLTPVIEKVPGEQSFVGOHAATGCVATATAQIMKYHN 60
QY 281 YPNKGLKDYTYTLSSNNPFNFHPKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 340
Db 61 YPNKGLKDYTYTLSSNNPFNFHPKNLFAAISTROYNNWNNILPTYSGRESNVQKMAISELM 120
QY 341 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 400
Db 121 ADVGISVDMYDGPSSGSGSSRVQRALKENFGYNQSVHQNRSDFSQDWEAQIDKELSON 180
QY 401 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 460
Db 181 QPVYQGGKVGGHAFVIDGADGRNFYHVNWGGVSDGFFRLDALNPSALGTGGGAGGFN 240
QY 461 GYQSAVVG 468
Db 241 GYQSAVVG 248

RESULT 6
AAW07898
ID AAW07898 standard; protein; 398 AA.
XX AC AAW07898;
XX DT 22-JUL-1997 (first entry)
XX DE Streptococcus pyogenes clone speB7 pre-pro cysteine protease.
XX KW Pre-pro; cysteine; protease; inhibition; neoplastic; proliferation; cell;
KW human; treatment; carcinoma; sarcoma; melanoma; lymphoma; leukaemia;
KW leukemia; blood; lung; mammary gland; prostate; intestine; stomach;
KW liver; heart; skin; pancreas; brain tissue; wound covering; prevention;
KW metastasis; identification; speB7.
XX OS Streptococcus pyogenes.
XX PH Key Location/Qualifiers
FT Misc-difference 216 /note= "corresponding codon TAG"
FT 333..338
FT Domain /label= nucleotide_binding_domain
XX PN WO9634941-A1.
XX PD 07-NOV-1996.
XX PF 30-APR-1996; 96WO-US005997.
XX PR 01-MAY-1995; 95US-00432692.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Musser JM, Kapur V, Ananthaaswamy H, Fernandez A;
XX WPI; 1996-506148/50.
XX DR N-PSDB; AAT45219.
XX PT Use of extracellular Streptococcal cysteine protease enzyme - for
XX PT inhibiting the proliferation of neoplastic cells, e.g. for treating
XX PT carcinoma, lymphoma or leukaemia.
XX PS Disclosure; Page 59-61; 99pp; English.

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RESULT 3
AAE37691
ID AAE37691 standard; protein; 468 AA.
AC AAE37691;
XX
XX
DT 06-OCT-2003 (first entry)
DE
DE S. pyogenes mature mutant SpeA-mature mutant SpeB fusion protein.
XX
XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
KW gene therapy; fusion protein; SpeB; mutant; mutein.
XX
XX Streptococcus pyogenes.
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Encoded by GCT"
FT
FT Misc-difference 42 /note= "Wild type Leu substituted with Arg"
FT Misc-difference 267
FT Misc-difference /note= "Wild type Cys substituted with Ser"
XX
XX WQ2003056015-A1.
XX
XX 10-JUL-2003.
XX
XX 26-NOV-2001; 2001WO-US046540.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
PA
PA Ulrich RG;
PI
XX
XX WPI; 2003-492125/46.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Example 14; Page; 141pp; English.
XX
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX mature mutant pyrogenic exotoxin A (SpeA)-mature mutant SpeB fusion
XX protein. This sequence is used in the invention. Note: This sequence is
XX not shown in the specification, but is derived from S. pyogenes mature
XX wild-type SpeA-SpeB protein (AAE37684)
XX
XX Sequence 468 AA;

Query Match 99.4%; Score 2484; DB 7; Length 468;
Best Local Similarity 99.6%; Pred. No. 1.4e-193;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDRSHDLIYNVSGPNYDKLK 60
DB 1 MQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDRSHDLIYNVSGPNYDKLK 60
QY 61 TELKNQEMATLFRKNDIYGVYHLCYLCEAERSACIGGVNREGNHLEIPKKIVVK 120
DB 61 TELKNQEMATLFRKNDIYGVYHLCYLCEAERSACIGGVNREGNHLEIPKKIVVK 120
QY 121 VSIDGQISLFSFIETNKKMWTQAQELDYKVRKYLTDNKLQYTNGPSKYETGYIKFIPKNKE 180
DB 121 VSIDGQISLFSFIETNKKMWTQAQELDYKVRKYLTDNKLQYTNGPSKYETGYIKFIPKNKE 180

181 SFWDFPFPEPTQSKYLMYYKDNETLDSNTQIEVYLTQKPVVKSLLDSKGHYNOGNP 240
181 SFWDFPFPEPTQSKYLMYYKDNETLDSNTQIEVYLTQKPVVKSLLDSKGHYNOGNP 240
241 YNLLTPVIEKVPGEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYF 300
241 YNLLTPVIEKVPGEQSFVQGHAAATGCVATATAQIMKYHNPKNKGLKDYTYTLSSNNPYF 300
301 NHPKNLFAAISTROYNWNNILPTYSGRESNVQKMAISELMADVIGISVDMDYGPSSGSAGS 360
301 NHPKNLFAAISTROYNWNNILPTYSGRESNVQKMAISELMADVIGISVDMDYGPSSGSAGS 360
361 SRVQALKENFGYNQSVHQNESDFSQDWEAIDKELSONQPVYQGGKVGGHAFVIDGA 420
361 SRVQALKENFGYNQSVHQNESDFSQDWEAIDKELSONQPVYQGGKVGGHAFVIDGA 420
421 DGRNFFVHNWGMGVSDGFFRLDALNPSALGTGGGAGGFGYQSAVVG 468
421 DGRNFFVHNWGMGVSDGFFRLDALNPSALGTGGGAGGFGYQSAVVG 468

RESULT 4
ABU62333
ID ABU62333 standard; protein; 248 AA.
XX
AC ABU62333;
XX
XX 27-AUG-2003 (first entry)
XX
XX Streptococcus pyrogenic toxin b, wild-type mature sequence.
XX
XX Streptococcus pyrogenic enterotoxin a; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
XX antibacterial.
XX
XX Streptococcus sp.
XX
XX US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Example 14; Page 42-43; 68pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection,
XX antisera isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SECl) and streptococcal pyrogenic enterotoxin a and b (SPEa and

```

```

PS Claim 10; Page 44-46; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded superantigen toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SpeA and
CC SpeB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the SpeA L42R/SpeB C47S mutant fusion protein. Note:
CC The present sequence is described as having the Cys to Ser mutation in
CC the SpeB portion at residue 267 (corresponding to amino acid 47 of mature
CC SpeB), but the residue is still Cys
XX
SQ Sequence 468 AA;
Query Match 100.0%; Score 2500; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.9e-195;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQQDPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
Db 1 MQQDPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
QY 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLIPKKIVVK 120
Db 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLIPKKIVVK 120
QY 121 VSIDGQISLFDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQISLFDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDSKGIHYNQGNP 240
Db 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDSKGIHYNQGNP 240
QY 241 YNLLTPVIEKVPGEQSFVQGHAAATGCATATATAQIMKYNHYPNKGDKDYTYTLSSNNPYF 300
Db 241 YNLLTPVIEKVPGEQSFVQGHAAATGCATATATAQIMKYNHYPNKGDKDYTYTLSSNNPYF 300
QY 301 NHPKNLFAAISTROYNNNLLPTYSGRESNVQKMAISELMADVIGISVDMDYGPSGSAGS 360
Db 301 NHPKNLFAAISTROYNNNLLPTYSGRESNVQKMAISELMADVIGISVDMDYGPSGSAGS 360
QY 361 SRVORALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGAHAFIDGA 420
Db 361 SRVORALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGAHAFIDGA 420
QY 421 DGRNFYHVNWGWGVSDFGFFRLDALNPSALGTGGGAGGFNGYSQSAVVG 468
Db 421 DGRNFYHVNWGWGVSDFGFFRLDALNPSALGTGGGAGGFNGYSQSAVVG 468

RESULT 2
AAE37684
ID AAE37684 standard; protein; 468 AA.
XX
AC AAE37684;
XX
DT 06-OCT-2003 (first entry)
XX
DE Streptococcus pyogenes SpeA-SpeB fusion protein.

```

```

XX Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
KW gene therapy; fusion protein; SpeB.
XX
OS Streptococcus pyogenes.
XX
PN WO2003056015-A1.
PD 10-JUL-2003.
XX
PF 26-NOV-2001; 2001WO-US046540.
XX
PR 26-NOV-2001; 2001US-00002784.
XX
PA (USNE-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Ulrich RG;
XX
WI 2003-492125/46.
XX
N-PSDB; AAD56778.
XX
DR New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
PS Claim 10; Page 134; 141pp; English.
XX
CC The invention provides a superantigen toxin DNA fragment which has been
CC genetically altered such that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is disrupted or
CC altered. DNA fragments of the invention are useful in the production of
CC vaccines against bacterial superantigen toxin infections. They are also
CC useful in gene therapy. The present sequence is Streptococcus pyogenes
CC pyrogenic exotoxin A (SpeA)-SpeB fusion protein. This sequence is used in
CC the invention
XX
SQ Sequence 468 AA;
Query Match 100.0%; Score 2500; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 6.9e-195;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQQDPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
Db 1 MQQDPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK 60
QY 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLIPKKIVVK 120
Db 61 TELKNQEMATLFDKKNIDYGVVEYHLCYLCEAERSACIGGVTNREGNHLIPKKIVVK 120
QY 121 VSIDGQISLFDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
Db 121 VSIDGQISLFDIETNKKQMTAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180
QY 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDSKGIHYNQGNP 240
Db 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTQIEVYLTQKPVKSLDSKGIHYNQGNP 240
QY 241 YNLLTPVIEKVPGEQSFVQGHAAATGCATATATAQIMKYNHYPNKGDKDYTYTLSSNNPYF 300
Db 241 YNLLTPVIEKVPGEQSFVQGHAAATGCATATATAQIMKYNHYPNKGDKDYTYTLSSNNPYF 300
QY 301 NHPKNLFAAISTROYNNNLLPTYSGRESNVQKMAISELMADVIGISVDMDYGPSGSAGS 360
Db 301 NHPKNLFAAISTROYNNNLLPTYSGRESNVQKMAISELMADVIGISVDMDYGPSGSAGS 360
QY 361 SRVORALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGAHAFIDGA 420
Db 361 SRVORALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPVYQGGKVGGAHAFIDGA 420
QY 421 DGRNFYHVNWGWGVSDFGFFRLDALNPSALGTGGGAGGFNGYSQSAVVG 468
Db 421 DGRNFYHVNWGWGVSDFGFFRLDALNPSALGTGGGAGGFNGYSQSAVVG 468

```

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OM protein - protein search, using sw model

Run on: September 17, 2005, 00:47:53 ; Search time 152.962 Seconds
(without alignments)
1183.322 Million cell updates/sec

Title: US-10-002-784A-27

Perfect score: 2500

Sequence: 1 MQQDPDPQLHRSLLVKNLQ.....ALGTGGGAGFNGYQSAVVG 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19808:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20038:*

8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2500	100.0	468	7 ABU62335	ABU62335 SPEa L42R
2	2500	100.0	468	7 AAE37684	AAE37684 Streptoco
3	2484	99.4	468	7 AAE37691	AAE37691 S. pyogen
4	1332	53.3	248	7 ABU62333	ABU62333 Streptoco
5	1332	53.3	248	7 AAE37686	AAE37686 Streptoco
6	1327.5	53.1	398	2 AAU07898	AAU07898 Streptoco
7	1327.5	53.1	398	2 AAR95856	AAR95856 S. pyogen
8	1327.5	53.1	398	3 AAY81812	AAY81812 S. pyogen
9	1327.5	53.1	398	8 ADP89840	ADP89840 Streptoco
10	1324.5	53.0	398	7 ABU62332	ABU62332 Streptoco
11	1323.5	52.9	398	5 ABP29579	ABP29579 Streptoco
12	1323.5	52.9	398	7 AAE37685	AAE37685 Streptoco
13	1323.5	52.9	398	8 ADR83971	ADR83971 S. pyogen
14	1322	52.9	248	7 AAE37690	AAE37690 S. pyogen
15	1195.5	47.8	398	3 AAB36098	AAB36098 Streptoco
16	1168	46.7	220	7 ABU62334	ABU62334 Streptoco
17	1168	46.7	220	7 AAE37687	AAE37687 Streptoco
18	1163	46.5	220	7 AAE37689	AAE37689 S. pyogen
19	1162	46.5	220	7 AAE37688	AAE37688 S. pyogen
20	1136	45.4	251	3 AAY70109	AAY70109 Streptoco
21	1136	45.4	251	5 ABB79508	ABB79508 Streptoco
22	1136	45.4	251	6 ABU10088	ABU10088 Streptoco
23	1136	45.4	251	7 ABU62331	ABU62331 Streptoco
24	1136	45.4	251	7 AAE37683	AAE37683 Streptoco
25	1130	45.2	251	7 ABU62460	ABU62460 Streptoco

ALIGNMENTS

RESULT 1

ABU62335
ID ABU62335 standard; protein; 468 AA.

XX AC ABU62335;

XX DT 27-AUG-2003 (first entry)

XX DE SPEa L42R/SPEB C47S mutant fusion protein.

XX KW SPEa; streptococcus pyrogenic enterotoxin; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial; SPEB.

XX OS Streptococcus sp.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 43 /label= Wild-type Leu substituted by Arg

FT Misc-difference 100. .101 /note= "Encoded by ATCTACGGA"

FT Misc-difference 211. .212 /note= "Encoded by ACNAGCCAA"

FT Misc-difference 386. .387 /note= "Encoded by AGCAAAACAA"

FT Misc-difference 407. .408 /note= "Encoded by GGTGTGGGT"

XX US2003036644-A1.

PD 20-FEB-2003.

XX 26-NOV-2001; 2001US-00002784.

XX 25-JUN-1997; 97US-00882431.

XX 01-SEP-1998; 98US-00144776.

XX (ULRI/) ULRICH R G.

XX Ulrich RG;

XX WPI; 2003-492125/46.

XX N-PSDB; ACD28908.

XX New superantigen toxin DNA fragment, useful for preparing a composition

XX for treating or preventing bacterial infection.

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Charles H. Harris
;; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
;; CITY: FORT DETRICK
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 21702-5012
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.5
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/882,431B
;; FILING DATE: June 25, 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Charles H. Harris
;; REGISTRATION NUMBER: 34,616
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 619-2065
;; TELEFAX: (301) 619-7714
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 266
;; TYPE: Amino Acid
;; STRANDEDNESS: Unknown
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: Peptide
;; US-08-882-431B-6

Query Match 42.9%; Score 567.5; DB 4; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.9e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19; Gaps 7;

Qy	15	VLVTFGLTIS-QEVEFA--QQDPDPQSOLHSSSLVKNL-QNIYFLEYEGDPVTHENVKSVQDQ	70
Db	11	ILIFALILVISTPNVLAESQDPKPDDELHKSKFTGLMEDMKVLYDDNHVSAINVKSIDQ	70
Qy	71	LRSHDLIYNVSGP---NYDKLTKELKNOEMATLFDKNVDIYGVVYHLCYLCENA----	123
Db	71	FLYFDLIYSIKDTKLGDDYDNVRVEFKKDLADKYKDYVDVFCGANYYYQCYFSKKTNDIN	130
Qy	124	-----ERSACIYGGVTHNEGNHLEIPKKIVKVSIDIGIOSLSFDIETNKQMTAQELDYK	178
Db	131	SHQTKRKTKCMYGGVTEHNGNQLDKYRSITVRVPEDEGKNLLSFDVQTNKKKVTQAELDYL	190
Qy	179	VRKYLTDNKOLYNGPSKYETGYIKFIPKNKESFWDFPPEP---EFTOSKYLMIYKDNET	236
Db	191	TRHYLVKNKKGLYEFNNSPYETGYIKFT-ENENSFWYDMMPAPGDKFAQSKYLLMMYNDKM	249
Qy	237	LDSENTQIEVYLTK 251	
Db	250	VDSKDVKIEVYLTK 264	

Search completed: September 17, 2005, 00:48:30
Job time : 14.9638 secs

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QY 124 --ERSACIYGGVTHNHEGNIETPKKIVVKVSDIGTQSLSFDIETNKKMVTAEQELDYKVRK 181
Db 123 TDKRKTCTMGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDYLTRH 182
QY 182 YLTDNKLQYTNKQYETGVIKFIKPKNESFWDFPPEP--EFTOSKYLMIYKDNETLDS 239
Db 183 YLVKVKLYEFNNSPYETGIKFI-ENENSWFYDMMPAFGDFDQSKYLMYNDNKNVDS 241
QY 240 NTSQIEVYLTTK 251
Db 242 KDVKIEVYLTTK 253

RESULT 13
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 43.5%; Score 575; DB 3; Length 266;
Best Local Similarity 47.2%; Pred. No. 3.5e-47;
Matches 125; Conservative 40; Mismatches 78; Indels 22; Gaps 8;
QY 8 LKXNVFF---VLVTFGLGLIIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPV 60
Db 1 MDKRLIFISHVILFALILVISTPNVLAESQDPKDELHKSKFTGLMENKVLXDNDHV 60
QY 61 THENKSVQLRSHDLIYNVSGP---NYDKLKTTELKQEMATLFXDKKNVDIYGVYHLC 117
Db 61 SAINVKSIDQSLYFDLIYSIKDTKLGNVDNRVFEKKNKDLADKYKDYVDVFGANYIQC 120
QY 118 YLCENA-----ERSACIYGGVTHNHEGNIETPKKIVVKVSDIGTQSLSFDIETNKK 168
Db 121 YFSKKTNDINSHQTKRKTCTMGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKK 180
QY 169 MYTAEQELDYKVRKYLTDNKLQYTNKQYETGVIKFIKPKNESFWDFPPEP--EFTQSK 226
Db 181 KVTAQELDYLTRHYLVKVKLYEFNNSPYETGIKFI-ENENSWFYDMMPAFGDFDQSK 239
QY 227 YLMIYKDNETLDSNTSQIEVYLTTK 251
Db 240 YLMYNDNKNVDSKDVKIEVYLTTK 264

RESULT 14
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 42.9%; Score 567.5; DB 3; Length 266;
Best Local Similarity 47.5%; Pred. No. 1.8e-46;
Matches 121; Conservative 40; Mismatches 75; Indels 19; Gaps 7;
QY 15 VLWTFGLTIS-QEVFA--QQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSDVQ 70
Db 11 ILIFALILVISTPNVLAESQDPKDELHKSKFTGLMEDMKVLYDDNHVSAINVKSIDQ 70
QY 71 LRSHDLIYNVSGP---NYDKLKTTELKQEMATLFXDKKNVDIYGVYHLCYLCENA---- 123
Db 71 FLYFDLIYSIKDTKLGDYDNRVFEKKNKDLADKYKDYVDVFGANYIYQCYFSKKTNDIN 130
QY 124 -----ERSACIYGGVTHNHEGNIETPKKIVVKVSDIGTQSLSFDIETNKKMVTAEQELDYK 178
Db 131 SHQTKRKTCTMGVTEHNGNQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDYL 190
QY 179 VRKYLTDNKLQYTNKQYETGVIKFIKPKNESFWDFPPEP--EFTOSKYLMIYKDNET 236
Db 191 TEHYLVKVKLYEFNNSPYETGIKFI-ENENSWFYDMMPAFGDFDQSKYLMYNDNKNV 249
QY 237 LDSNTSQIEVYLTTK 251
Db 250 VDSKDVKIEVYLTTK 264

RESULT 15
US-08-882-431B-6
; Sequence 6, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25

```
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: Fast-SEQ for Windows Version 3.0
/ SEQ ID NO 20
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match          74.1%; Score 979.5; DB 4; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPQLHRSGLVKNLQNIYFLYEGDPVTHENVKSVDPQLRSHDLIYVSGPNYDKLTCLK 93
Db 4 PRESQQRSLVNTFKIYIFFMRVTLVTHENVKSVDPQLRSHDLIYVSGPNYDKLTCLK 63

QY 94 NQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNLEIPKIVVKVSI 153
Db 64 NQEMATLFDKKNVDIYGVVEYHLCYLCENASACIYGGVTNHEGHNLEIPKIVVKVSI 123

QY 154 DGIQSLSPDIETNKKMWTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 213
Db 124 DGIQSLSPDIETNKKMWTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251
Db 183 FDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTTK 220

RESULT 11
US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match          44.5%; Score 588; DB 1; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFGLTISQEVFAQDDPDPQLHRSGLVKNL-QNIYFLYEGDPVTHENVKSVDPQLRS 73
Db 3 MITNLIRLTIGNSMESQDPKPKDELHKSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYVNSGP---NYDKLKTLEKNQEMATLFDKKNVDIYGVVEYHLCYLCENA----- 123
Db 63 FDLIYSIKDTKLGNDVNRVFEKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQ 122

QY 124 --ERSACIYGGVTNHEGHNLEIPKIVVKVSI DGIQSLSPDIETNKKMWTQAELDYKVRK 181
Db 123 TDKRKTCVMYGGVTEHNGNQLDKYRSITVRVFEDEGKNLLSFDVQTNKKKVTQAELDYLTRH 182

QY 182 YLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPPEP--EFTQSKYLMYKDNETLDS 239
Db 183 YLVKKNKLYEFNNSPYETGYIKFI-ENENSWFYDMMWPAFGDPQSKYLMYNDNKNQVDS 241

QY 240 NTSQIEVYLTTK 251
Db 242 KDVKIEVYLTTK 253

RESULT 12
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935588
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-2

Query Match          44.5%; Score 588; DB 2; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.9e-48;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFGLTISQEVFAQDDPDPQLHRSGLVKNL-QNIYFLYEGDPVTHENVKSVDPQLRS 73
Db 3 MITNLIRLTIGNSMESQDPKPKDELHKSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYVNSGP---NYDKLKTLEKNQEMATLFDKKNVDIYGVVEYHLCYLCENA----- 123
Db 63 FDLIYSIKDTKLGNDVNRVFEKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQ 122
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; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match      88.0%; Score 1163; DB 4; Length 221;
Best Local Similarity 99.1%; Pred. No. 8.7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVNSGPNYDKLKT 90
DB 1 QDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVNSGPNYDKLKT 60

QY 91 ELKNQEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVK 150
DB 61 ELKNQEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVK 120

QY 151 VSDIGTQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKE 210
DB 121 VSDIGTQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKE 180

QY 211 SFWFDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWFDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 8
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match      74.1%; Score 979.5; DB 3; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVNSGPNYDKLTK 93
DB 4 PKPSQLQRSNLVTKFIYFFMRVTLVTHENVKSDQLRSHDLIYVNSGPNYDKLTK 63

QY 94 NOEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVKVSI 153
DB 64 NOEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVKVSI 123

QY 154 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 213
DB 124 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 10
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
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QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 9
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match      74.1%; Score 979.5; DB 3; Length 220;
Best Local Similarity 86.7%; Pred. No. 3.7e-86;
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;

QY 34 PDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYVNSGPNYDKLTK 93
DB 4 PKPSQLQRSNLVTKFIYFFMRVTLVTHENVKSDQLRSHDLIYVNSGPNYDKLTK 63

QY 94 NOEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVKVSI 153
DB 64 NOEMATLFDKKNVDIYGVYHYHLCYLCAERASACIYGGVTNHEGHNHLEIPKKIVVKVSI 123

QY 154 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 213
DB 124 DGIQSLSFDETNNKMWTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKNKESFW 182

QY 214 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 183 FDFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 220

RESULT 10
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
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US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match 88.0%; Score 1164; DB 3; Length 221;
Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 5
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29
Query Match 88.0%; Score 1164; DB 3; Length 221;

Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 6
US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-29

Query Match 88.0%; Score 1164; DB 4; Length 221;
Best Local Similarity 99.1%; Pred. No. 7e-104;
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 90
DB 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVLDLRSHDLIYNVSGPNYDKLKT 60
QY 91 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 150
DB 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVVK 120
QY 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210
DB 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 251
DB 181 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTK 221

RESULT 7
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas

Best Local Similarity 100.0%; Pred. No. 5.6e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
US-08-882-431B-16
; Sequence 16, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MWC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-16

Query Match 100.0%; Score 1322; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.6e-119;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 3
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USNO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PPT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 98.9%; Score 1308; DB 4; Length 251;
Best Local Similarity 99.2%; Pred. No. 1.2e-117;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQWFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKQEMATLFDKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDIGIQSLSPDIETNKKQWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 00:42:17 ; Search time 13.9638 Seconds
(without alignments)
1341.817 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MNNKKVLKMKVFFVLVTFL.....KDNETLDSNTSQIEVLTITK 251

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfilese1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1322	100.0	251	4	US-08-882-431B-16
3	1308	98.9	251	4	US-08-973-391C-13
4	1164	88.0	221	3	US-08-896-933-29
5	1164	88.0	221	3	US-09-314-235-29
6	1164	88.0	221	4	US-09-708-008B-29
7	1163	88.0	221	4	US-08-973-391C-14
8	979.5	74.1	220	3	US-08-896-933-20
9	979.5	74.1	220	3	US-09-314-235-20
10	979.5	74.1	220	4	US-09-708-008B-20
11	588	44.5	255	1	US-08-446-918A-2
12	588	44.5	255	2	US-08-580-806-2
13	575	43.5	266	3	US-09-414-276-8
14	567.5	42.9	266	3	US-09-144-776B-6
15	567.5	42.9	266	4	US-08-882-431B-6
16	563	42.6	239	3	US-09-144-776B-10
17	563	42.6	239	4	US-08-882-431B-10
18	561	42.4	239	3	US-08-896-933-26
19	561	42.4	239	3	US-09-314-235-26
20	561	42.4	239	4	US-09-708-008B-26
21	558.5	42.2	266	3	US-09-144-776B-8
22	558.5	42.2	266	4	US-08-882-431B-8
23	553	41.8	266	3	US-09-144-776B-14
24	553	41.8	266	4	US-08-882-431B-14
25	545	41.2	238	3	US-08-896-933-28
26	545	41.2	238	3	US-09-314-235-28
27	545	41.2	238	4	US-09-708-008B-28

28	544	41.1	239	3	US-08-896-933-27	Sequence 27, Appl
29	544	41.1	239	3	US-09-314-235-27	Sequence 27, Appl
30	544	41.1	239	4	US-09-708-008B-27	Sequence 27, Appl
31	522	39.5	239	3	US-08-896-933-21	Sequence 21, Appl
32	522	39.5	239	3	US-09-314-235-21	Sequence 21, Appl
33	522	39.5	239	4	US-09-708-008B-21	Sequence 21, Appl
34	424	32.1	79	3	US-09-144-776B-24	Sequence 24, Appl
35	424	32.1	79	4	US-08-882-431B-24	Sequence 24, Appl
36	328.5	24.8	228	3	US-08-896-933-25	Sequence 25, Appl
37	328.5	24.8	228	4	US-09-314-235-25	Sequence 25, Appl
38	328.5	24.8	228	4	US-09-708-008B-25	Sequence 25, Appl
39	308	23.3	257	3	US-08-486-099-112	Sequence 112, App
40	308	23.3	257	3	US-08-360-107A-122	Sequence 122, App
41	308	23.3	257	3	US-08-484-223B-112	Sequence 112, App
42	308	23.3	257	3	US-08-919-597-112	Sequence 112, App
43	308	23.3	257	3	US-08-475-668A-112	Sequence 112, App
44	308	23.3	257	3	US-08-485-551A-112	Sequence 112, App
45	308	23.3	257	3	US-08-471-913A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16
Query Match 100.0% Score 1322; DB 3; Length 251;


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DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C; 1.
DR Pfam; PF01123; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
KW Supranatigen; Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type B.
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT STRAND 209 218
FT TURN 221 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 4.4e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS--QDDPDPSQLHRSSLVKML-QNIYFLYEGDPVTHENVKSV 70
DB 11 ILIFALLIVSTNVLAEQDPDKDELHKSKFTGLMENKMKVLYDDNHVSALNVKSIDQ 70

QY 71 LRSHDLIYNVSGP---NYDKLKTGLKQEMATLFDKNVDIYGVYHYLCYLCEA----123
DB 71 FLYFDLIYSIKDTKLGNDYDNRVFEKNGKOLADKYDKYDVFNGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTNHEGHNLEIPKIVVKVSDIGIQSLSPDIETNKKWVTAQELDYK 178

DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C; 1.
DR Pfam; PF01123; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
KW Supranatigen; Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type B.
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT HELIX 184 199
FT STRAND 209 218
FT TURN 221 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 4.4e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS--QDDPDPSQLHRSSLVKML-QNIYFLYEGDPVTHENVKSV 70
DB 11 ILIFALLIVSTNVLAEQDPDKDELHKSKFTGLMENKMKVLYDDNHVSALNVKSIDQ 70

QY 71 LRSHDLIYNVSGP---NYDKLKTGLKQEMATLFDKNVDIYGVYHYLCYLCEA----123
DB 71 FLYFDLIYSIKDTKLGNDYDNRVFEKNGKOLADKYDKYDVFNGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTNHEGHNLEIPKIVVKVSDIGIQSLSPDIETNKKWVTAQELDYK 178

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OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9953269;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 8.4e-71;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISQVEFAQQDPDSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 80
DB 1 GLTTSQVEFAQQDPNSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 60

QY 81 SGNPYDKLTTELKXQEMATLFDKNVDIYGVYYHLCYLCENARSACIYGGVTNHEGNH 140
DB 61 SGLNYDKLTTELKXNREMTLFDKNVDIYGVYYHCHYLCKNAKRACIYGGVTNHEGNH 120

QY 141 LEIPKIVKVSIDGTSQSLFSDIETKKNWTAQELDYKVKYLTNDKNLYTNGPSKYETG 200
DB 121 LEIPKIVKVSIDGTSQSLFSDIETSKKNWTAQELDYKVKYLTNDKNLYTNGPSKYETG 180

QY 201 YIKFIPKNKESFWDFPFPPPEFTOSKYLMIYKDNETLDSNTS 242
DB 181 YIKFISKDKETFWDFPFPPPEFQVQVLYMIYKDNETLDSSTS 222

RESULT 12
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN Name:entB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
[2]
RP SEQUENCE OF 40-91 FROM N.A.

RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia
RT coli and Staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
[3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin B,
RT and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
[4]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806(1992).
[5]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RP MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
RA Jardtetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
[6]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RP MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
RA Li H., Ilera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
[7]
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RP MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M11118; AAA88550.1; -.
DR FIR; S27360; ENSAB6.
DR PDB; 1D5M; X-ray; C=28-266.
DR PDB; 1D5X; X-ray; C=28-266.
DR PDB; 1D5Z; X-ray; C=28-266.
DR PDB; 1D6E; X-ray; C=28-266.
DR PDB; 1SBB; X-ray; B/D=28-266.
DR PDB; 1SE3; X-ray; @=28-266.
DR PDB; 1SE4; X-ray; @=28-266.
DR PDB; 1SEB; X-ray; D/H=29-262.
DR PDB; 2SEB; X-ray; D=28-266.
DR PDB; 3SEB; X-ray; @=28-266.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.

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Qy 69 DQLRSHDLIYVSGPNYDKLTKEKNOEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 128
Db 61 DQLLSDHDLIYVSGPNYDKLTKEKNOEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 120

Qy 129 IYGGVTNHEGNHLEIPKKIIVKVSIDGIIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 188
Db 121 IYGGVTNHEGNHLEIPKKIIVKVSIDGIIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 180

Qy 189 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYL 228
Db 181 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYL 220

RESULT 9
Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL, X61573; CAA43771.1; -.
DR F1R; S18789; S18789.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 83.9%; Score 1109; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 7.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 9 KKMVFVLTFLGLTISQVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKIIVFLAIFGLTISQVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

Qy 69 DQLRSHDLIYVSGPNYDKLTKEKNOEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 128
Db 61 DQLLSDHDLIYVSGPNYDKLTKEKNOEMATLFKDKNVDIYGVYVHLCYLCEAERSAC 120

Qy 129 IYGGVTNHEGNHLEIPKKIIVKVSIDGIIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 188
Db 121 IYGGVTNHEGNHLEIPKKIIVKVSIDGIIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNKK 180

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Qy 189 LYTGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTGPSKYETGYIKFISKDKETFWDFPPEFNQVKYLMYKDNETLDSNTSQI 236

RESULT 10
Q938P4 PRELIMINARY; PRT; 222 AA.
AC Q938P4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=12620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
RL FEMS Microbiol. Lett. 219:291-295 (2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
FT NON_TER 222
SQ SEQUENCE 222 AA; 25984 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 8.4e-71;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 21 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 80
Db 1 GLTTSQEVFAQQDDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYV 60

Qy 81 SGPYVDKLTKEKNOEMATLFKDKNVDIYGVYVHLCYLCEAERSACIYGVVTHNEGNH 140
Db 61 SGLNYDKLTKEKNOEMSTLFKNKNVDIYGVYVHLCYLCRNARRACIYGVVTHNEGNH 120

Qy 141 LEIPKKIIVKVSIDGIIQSLSFDIETNKKMVTQAQLDYKVRKYLTDNQLYTGPSKYETG 200
Db 121 LEIPKNILVKSIDGIIQSLSFDIETSKMVTQAQLDYKVRKHLTDNNQLYTGPSKYETG 180

Qy 201 YIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTS 242
Db 181 YIKFISKDKETFWDFPPEFNQVKYLMYKDNETLDSNTS 222

RESULT 11
Q9S5Z4 PRELIMINARY; PRT; 222 AA.
AC Q9S5Z4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Exotoxin type A (Fragment).
GN Name=speA;

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DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR02876; Staph_Strep_tox_C; 1.
DR PROSITE; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; 2EF7F41AACB53600 CRC64;

Query Match 93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 3.4e-84;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASRSAC 128
Db 61 DQLSHDLIYVSGPNYDKLTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASRSAC 120

QY 129 IYGVVTHHGNHLEIPKKIIVKVSIDGIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 188
Db 121 IYGVVTHHGNHLEIPKKIIVKVSIDGIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 180

QY 189 LYTNGPSKYETGVIKIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTNGPSKYETGVIKIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 7
Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF055698; AAD11624.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
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SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 88.7%; Score 1173; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 1.1e-79;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLASHDLIYV 80
Db 1 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVVDQLASHDLIYV 60

QY 81 SGPNYDKLTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASRSACIYGGVTHHGNH 140
Db 61 SGPNYDKLTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASRSACIYGGVTHHGNH 120

QY 141 LEIPKKIIVKVSIDGIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQIYTGPSKYETG 200
Db 121 LEIPKKIIVKVSIDGIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQIYTGPSKYETG 180

QY 201 YIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTS 242
Db 181 YIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTS 222

RESULT 8
Q9A9Q0 PRELIMINARY; PRT; 220 AA.
AC Q9A9Q0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selanders R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61554; CAA43752.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >220 type A exotoxin.
FT NON_TER 220 220
SQ SEQUENCE 220 AA; 25600 MW; 92DB096E57906DF6 CRC64;

Query Match 87.7%; Score 1159; DB 2; Length 220;
Best Local Similarity 99.5%; Pred. No. 1.2e-78;
Matches 219; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60
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DR GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Pfam: PF02876; Staph_strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Signal.
DR NON_TER 1 1
DR SIGNAL <1 22 Potential.
DR CHAIN 23 >236 type A exotoxin.
DR NON_TER 236 236
DR SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 93.8%; Score 1240; DB 2; Length 236;
Best Local Similarity 99.6%; Pred. No. 1.2e-84;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 68
DB 1 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 128
DB 61 DQLLSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 120

QY 129 IYGVVTHNEGNHLEIPKLIYVKSIDIGISLFDIETNKKMTAQELDYKVRKYLTDNKK 188
DB 121 IYGVVTHNEGNHLEIPKLIYVKSIDIGISLFDIETNKKMTAQELDYKVRKYLTDNKK 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 5
Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54613; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS485, MGAS158, MGAS491, MGAS495, and MGAS624;
RC MEDLINE=92044323; PubMed=1940804;
RX Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61569; CAA43767.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR EMBL; X61572; CAA43770.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO:0005576; C:extracellular; IEA.
DR GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.

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DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Signal.
DR NON_TER 1 1
DR SIGNAL <1 22 Potential.
DR CHAIN 23 >236 type A exotoxin.
DR NON_TER 236 236
DR SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 93.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 1.4e-84;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 68
DB 1 KMWFFVLVTFLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLRSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 128
DB 61 DQLLSHDLIYVNGPNYDKLTTELKNQEMATLFDKNVDIYGVYHYHLCYLCEAERSAC 120

QY 129 IYGVVTHNEGNHLEIPKLIYVKSIDIGISLFDIETNKKMTAQELDYKVRKYLTDNKK 188
DB 121 IYGVVTHNEGNHLEIPKLIYVKSIDIGISLFDIETNKKMTAQELDYKVRKYLTDNKK 180

QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 6
Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, MGAS250, MGAS256, MGAS285, MGAS480, MGAS492, and MGAS496;
RC MEDLINE=92044323; PubMed=1940804;
RX Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR EMBL; X61567; CAA43765.1; -
DR PIR; A60108; A60108.
DR HSP; P01552; ISEB.
DR GO:0005576; C:extracellular; IEA.
DR GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.

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FT STRAND 197 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 251
SQ SEQUENCE 251 AA; 29246 MW; 54001FB4CCBFC3 CRC64;

Query Match 99.5%; Score 1315; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-90;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
Db |||||||
1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFXDKNVDIYGVYHYHLCYL 120
Db |||||||
61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFXDKNVDIYGVYHYHLCYL 120

QY 121 ENAERSACIYGGVTHNEGNHLEIPKKIYVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
Db |||||||
121 ENAERSACIYGGVTHNEGNHLEIPKKIYVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
Db |||||||
181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
Db |||||||
241 TSQIEVYLTTK 251

RESULT 3
O8K6K5 PRELIMINARY; PRT; 251 AA.
ID O8K6K5 Q79XZ6;
AC O8K6K5; 079XZ6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Exotoxin type A-phage associated (SpeA precursor).
GN Name=SpeA3; OrderedLocusNames=SP0560, SPYMJ_1301;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]_TaxID=198466;
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okabeashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
DR EMBL; AF014161; AAM79908.1; -.
DR EMBL; AF005142; BAC63655.1; -.

DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Stap/Strep toxin.
DR Pfam; PF01123; Stap_strip_toxin; 1.
DR Pfam; PF02876; Stap_strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN-
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCDS CRC64;

Query Match 99.4%; Score 1314; DB 2; Length 251;
Best Local Similarity 99.2%; Pred. No. 3.9e-90;
Matches 249; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
Db |||||||
1 MENNKKVLKKNVFFVLVTFGLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFXDKNVDIYGVYHYHLCYL 120
Db |||||||
61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFXDKNVDIYGVYHYHLCYL 120

QY 121 ENAERSACIYGGVTHNEGNHLEIPKKIYVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180
Db |||||||
121 ENAERSACIYGGVTHNEGNHLEIPKKIYVVKVSDIGIQSLSFDIETNKKMVTQAQELDYKVR 180

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240
Db |||||||
181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYIKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
Db |||||||
241 TSQIEVYLTTK 251

RESULT 4
P97163 PRELIMINARY; PRT; 236 AA.
ID P97163 P97164;
AC P97163; P97164;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (fragment).
GN Name=SpeA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS165, MGAS327, MGAS493, MGAS494, MGAS167, and MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Salsander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61556; CAA43754.1; -.
DR EMBL; X61555; CAA43753.1; -.
DR EMBL; X61557; CAA43755.1; -.
DR EMBL; X61558; CAA43756.1; -.
DR EMBL; X61559; CAA43757.1; -.
DR EMBL; X61560; CAA43758.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.

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KW Complete proteome; Signal; Toxin.
FT SIGNAL 1 30 By similarity.
FT CHAIN 31 251 Exotoxin type A.
FT DISULFID 117 128 By similarity.
SQ SEQUENCE 251 AA; 29246 MW; 54001FB4CCBFC3 CRC64;

Query Match 99.5%; Score 1315; DB 1; Length 251;
Best Local Similarity 99.6%; Pred. No. 3.3e-90;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNKKVLKVMFFVLVTLGTISQEVFAQDDPPSQRSLRVKLNQNIYFLYEGDVP 60
Db 1 MENNKKVLKVMFFVLVTLGTISQEVFAQDDPPSQRSLRVKLNQNIYFLYEGDVP 60

QY 61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYYHLCYLC 120
Db 61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKNOEMATLFDKKNVDIYGVYYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKIVVKVSDIGIQSLSFDIETNKKQWTAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKIVVKVSDIGIQSLSFDIETNKKQWTAQELDYKVR 180

QY 181 KYLTDNKQLYNTGSPSKYETGIKFIKPNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYNTGSPSKYETGIKFIKPNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTK 251
Db 241 TSQIEVYLTK 251

RESULT 2
SPEA_STRPY STANDARD; PRT; 251 AA.
AC P62560; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italian J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.

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CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta chain.

CC -!- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

CC -----

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CC -----

CC EMBL; U40453; AAC48868.1; -.

CC EMBL; X03929; CAA27568.1; -.

CC PIR; A26152; A26152.

CC PDB; 1B1Z; X-ray; -.

CC PDB; 1FNU; X-ray; -.

CC PDB; 1FNV; X-ray; -.

CC PDB; 1FNW; X-ray; -.

CC PDB; 1HA5; X-ray; -.

CC PDB; 1LOX; X-ray; -.

CC InterPro; IPR008992; Bact_endotox.

CC InterPro; IPR006177; Bctrl_tox.

CC InterPro; IPR006123; Staph/Strep_toxin.

CC InterPro; IPR006126; Staph/Strep_tox.

CC InterPro; IPR006173; Staph_tox_OB.

CC Pfam; PF02876; Staph_strep_tox_C; 1.

CC Pfam; PF01123; Staph_strep_toxin; 1.

CC PRINTS; PR00279; BACTRLTOXIN.

CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

CC 3D-structure; Signal; Toxin.

FW SIGNAL 1 30

FT CHAIN 31 251 Exotoxin type A.

FT DISULFID 117 128

FT CONFLICT 6 6

FT CONFLICT 17 18 K -> E (in Ref. 2).

FT CONFLICT 25 35 VT -> MK (in Ref. 2).

FT CONFLICT 40 40 SQEVFAQDDP -> LPRGICSTRPK (in Ref. 2).

FT CONFLICT 43 43 H -> Q (in Ref. 2).

FT CONFLICT 47 59 S -> N (in Ref. 2).

FT CONFLICT 129 129 NLQNIYFLYEGDP -> TKIYIFPMRVTL (in Ref. 2).

FT CONFLICT 165 178 I -> L (in Ref. 2).

FT CONFLICT 165 178 TNKGWTAQELDYK -> QIKNGNCSRISYT (in Ref. 2).

FT TURN 36 38

FT HELIX 42 44

FT TURN 46 48

FT HELIX 49 56

FT STRAND 60 65

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 78

FT STRAND 82 82

FT TURN 83 84

FT STRAND 85 85

FT STRAND 87 91

FT HELIX 95 102

FT TURN 103 103

FT STRAND 106 110

FT STRAND 113 113

FT TURN 115 116

FT TURN 121 122

FT STRAND 126 130

FT STRAND 133 135

FT TURN 137 138

FT STRAND 140 153

FT TURN 154 155

FT STRAND 156 167

FT STRAND 169 171

FT HELIX 172 186

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 00:48:38 ; Search time 79.5939 Seconds
(without alignments)
1614.846 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MENNKKVLKMWFFVLVTFLL.....KNETILDSNTSQIEVYLITK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	99.5	251	1 SPEA_STRP8	P62561 streptococ
2	1315	99.5	251	1 SPEN_STRPY	P62560 streptococ
3	1314	99.4	251	2 Q8K6K5	Q8K6K5 streptococ
4	1240	93.8	236	2 P97163	P97163 streptococ
5	1239	93.7	236	2 Q54779	Q54779 streptococ
6	1234	93.3	236	2 Q57453	Q57453 streptococ
7	1173	88.7	222	2 Q9R931	Q9R931 streptococ
8	1159	87.7	220	2 Q79AQ0	Q79AQ0 streptococ
9	1109	83.9	236	2 Q54696	Q54696 streptococ
10	1054	79.7	222	2 Q938P4	Q938P4 streptococ
11	1054	79.7	222	2 Q9S5Z4	Q9S5Z4 streptococ
12	576.5	43.6	266	1 ETXB_STAAM	P01552 staphylococ
13	555	42.0	271	2 Q9F0L6	Q9F0L6 staphylococ
14	553	41.8	266	2 Q8NXXJ6	Q8NXXJ6 staphylococ
15	551.5	41.7	266	1 ETC3_STAAM	P23313 staphylococ
16	551	41.7	239	2 Q63678	Q63678 staphylococ
17	550	41.6	239	2 Q06532	Q06532 staphylococ
18	549	41.5	239	2 Q06533	Q06533 staphylococ
19	549	41.5	266	1 ETC2_STAAM	P34071 staphylococ
20	548	41.5	239	2 Q05157	Q05157 staphylococ
21	548	41.5	239	2 Q06531	Q06531 staphylococ
22	548	41.5	266	1 ETC1_STAAM	P01553 staphylococ
23	545	41.2	239	2 Q6ST49	Q6ST49 staphylococ
24	544	41.1	239	2 Q06535	Q06535 staphylococ
25	539	40.8	239	2 Q06534	Q06534 staphylococ
26	538	40.7	234	2 Q9R5X4	Q9R5X4 staphylococ
27	536.5	40.6	260	2 Q54971	Q54971 streptococ
28	531.5	40.2	260	2 Q54738	Q54738 streptococ
29	531.5	40.2	260	2 Q79X14	Q79X14 streptococ
30	531.5	40.2	260	2 Q54739	Q54739 streptococ
31	527	39.9	259	2 Q76LS8	Q76LS8 staphylococ

32	522	39.5	264	2	Q764P6	Q764P6 staphylococ
33	512.5	38.8	259	2	Q936G4	Q936G4 staphylococ
34	505	38.2	222	2	Q6XZE6	Q6XZE6 staphylococ
35	501	37.9	222	2	Q6XZE7	Q6XZE7 staphylococ
36	501	37.9	261	2	Q6XXM5	Q6XXM5 staphylococ
37	499	37.7	261	2	Q6YCN4	Q6YCN4 staphylococ
38	499	37.7	261	2	Q6GFN0	Q6GFN0 staphylococ
39	490	37.1	261	2	Q6XXM3	Q6XXM3 staphylococ
40	487	36.8	261	2	Q6XXM4	Q6XXM4 staphylococ
41	481	36.4	258	1	ETXG_STAAM	ETXG_STAAM staphylococ
42	472	35.7	258	2	Q6GFN2	Q6GFN2 staphylococ
43	471	35.6	258	2	Q9EZM3	Q9EZM3 staphylococ
44	471	35.6	258	2	Q9ZNF2	Q9ZNF2 staphylococ
45	470	35.6	214	2	Q6XZE8	Q6XZE8 staphylococ

ALIGNMENTS

RESULT 1

SPEA_STRP8
ID SPEA_STRP8 STANDARD; PRT; 251 AA.
AC P62561; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=speA; OrderedLocusNames=spyM18_0193;
OS Streptococcus pyogenes (serotype M18)
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RA "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever (By similarity).
CC
-!- SUBUNIT: Binds to major histocompatibility complex class II beta chain (By similarity).
CC
-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

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EMBL; AE009982; AAL97141.1; --
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bctrl_tox.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006126; Staph/Strep_cox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Staph_strp_tox_C; 1.
Pfam; PF01123; Staph_strp_toxin; 1.
PRINTS; PR00279; BACTRLTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

```
Best Local Similarity 34.1%; Pred. No. 1.2e-17;
Matches 91; Conservative 52; Mismatches 86; Indels 38; Gaps 13;

QY 10 KMVFFVLVTFLGLTI-----SQEVFAQQDDPSQLHRSSLVKLNQNIYELYEGD 58
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
5 KKTTFILLTIALTLITSPFVNCSEKSEERNGDLQKXSELOQTAL--SNDRQYY-HNGS 62
QY 59 PVTHENVKSDQLRSHDLIYN--VSGPN-YDKLTELKNOEMATLFXDKKNVDIYGVVEYH 115
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
63 AII-ENKESNDQFLKNTILFNDFTHQWYNDLLVDLGSKDTANIYKGGKVDLYGVVY-- 119
QY 116 LCYLCENAE--RSACIYGVGTHNHEGNHLEIPKKIVKVSIDGIQSL---SPDIETNKKWVT 171
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
120 -GYQCTCGTFFKACMYGGVTLHDNNQLEEEKVPINLWDGKQNTVPLGTIVKTNKKEVT 178
QY 172 AQELDYKVRKYLTDNKOLYT---NGPSKYETGYKFIKPKNKSFWDFPEPEFTQSKY 227
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
179 VQELDLQSRHYLHETNYLNTDAFNG--KIQGLIEFHPSSGDSGVGYDLFG----AQQY 232
QY 228 ----LMIYKDNETLDSNTSQIEVLYTT 250
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
233 PDTQLRIYRDNKTIKSKNMHIDIYLYT 259

RESULT 15
H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: UNIPROT:Q9EZM4; GB:BA000018; PID:gl3701618; PIDN:BA842911.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: sen
C;Superfamily: enterotoxin B

Query Match 23.6%; Score 311.5; DB 2; Length 258;
Best Local Similarity 33.8%; Pred. No. 7.5e-16;
Matches 89; Conservative 49; Mismatches 102; Indels 23; Gaps 10;

QY 1 MNNKKVLKKMVPF--VLVTFGLTISQEVFAQQD---PDPSQLHRSSLVKLNQNIY- 52
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1 MKIIKLMR--LFVIAIITLCLINNVTVAEVDKOLKKSDLDSSKLF-NLTSYTT 57
QY 53 -FLYEGDPVTHENVKSDQLRSHDLI---YNVSGPNYDKLTELKNOEMATLFXDKKNVDI 108
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58 DITWQLD---ESNKISTQLLNTIILKNIDISVLKTSLSKVEFNSSDLANQFKGNIDI 114
QY 109 YGVEYHYLCY-LCENAEASACIYGVGTHNHEGNHLEIPKKIVKVSIDGIQSLSFDIETNK 167
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
115 YGLYFGNKKCVGLTE--EKTSCLYGGVTIHDGNQLDEEKVIGVNVFKDGVQOQEGFVIKTK 172
QY 168 KMTAQLDYKVRKYLTDNKOLYTNGPSKYETGYKFIKPN--KESFWDFPEPEFTQS 225
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
173 AKVTVQELDTKVRPKLENLYKNKDTGNTQKGCIFPHSHHQDQSPYDLYNVKGSVGA 232
QY 226 KYLMIYKDNETLDSNTSQIEVYL 248
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
233 EFPQFYSNRTVSSNVHIDVFL 255

Search completed: September 17, 2005, 01:14:33
Job time : 19.153 secs
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C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33953
R;Bayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A;Reference number: A33953; MUID:89359112; PMID:2549000
A;Accession: A33953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <BAY>
A;Cross-references: UNIPROT:P20723; GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g75869
C;Superfamily: enterotoxin B

Query Match 25.7%; Score 340; DB 2; Length 258;
Best Local Similarity 35.2%; Pred. No. 5.9e-18;
Matches 92; Conservative 47; Mismatches 102; Indels 20; Gaps 10;

QY 8 LKWM-VFFVLVTLPLGLTISQ-EVFAQDDP---PSQLHR-----SSLVKNLQNIYFLYEG 57
DB 1 MKKFNILIALFFTSVLISPLNVKANENIDSVKEKSLHKKSELSSTALNNMKHSY--ADK 58
QY 58 DPVTHENVKSVQDLGRSHDIYN---VSGPNYDKLKTTELKNOEMATLFDKQNDVDIYGVYY 114
DB 59 NPIIGENKSTGDFLENTLLYKFFDLDLINFENFSKEMAQHFKSKQNDVYPIRYS 118
QY 115 HLCYLCENABERSACIYGGVTNHEGHNHLEIPKKIIVKVSIDGIQ-SLSFD-IETNKKMVTVA 172
DB 119 INCYGGE-IDRTACTYGGVTPHEGKLERKKIPINLWINGVQKEVSLDKVQTDKKNVTV 177
QY 173 QELDYKVRKYLTDNKKQLYNGP--SKYETGYIKFIPKNKESFWDFPFPEFTQSKYLM 230
DB 178 QELDAQARRYLRQDLKLYNNDTLGGKIQRGKIEFSDSGSKVSYDLFDVKGDPPEQLRI 237
QY 231 YKDNETLDSNTSOIEVLTTK 251
DB 238 YSDNKLSTLHLDIYLYEK 258

RESULT 12
E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q99T46; GB:BA000018; PID:g13701623; PIDN:BAB42916.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: seo
C;Superfamily: enterotoxin B

Query Match 25.6%; Score 338; DB 2; Length 260;
Best Local Similarity 36.2%; Pred. No. 8.4e-18;
Matches 96; Conservative 42; Mismatches 107; Indels 20; Gaps 9;

QY 1 MENKKVYKQVFPVLVTFGLTISQEVFA-QQDDPPFSQLHRSLLVK--NLQNIYFLYEG 57
DB 1 MKNSKWLNL--VLLILLNLIAICSVNNAYANEDPKIESLCKKSSVDPIALHNINDIYN 58
QY 58 DPVTHENVKSV-----DQLRSHDIYN-----VSG--PNYDKLKTTELKNOEMATLFDKQNDV 107
DB 59 NREFT--TVKSIIVSTTEKFLDFDLFLFKSINWLDGISAEFKDLKVEFSSSAISKEFLGKTVD 116
QY 108 IYGVYYHLCYLCENABERSACIYGGVTNHEGHNHLEIPKKIIVKVSIDGIQSLSFDIETNK 167

DB 117 IYGVYIKAHCH-GEHQVDTACTYGGVTPHENNKULSEPKNIGVAVYKDNVNVNFIUTDK 175
QY 168 KMTVTAQELDYKVRKYLTDNKKQLYNGPSKYETGYIKF--IPKNKESFWDFPFPEFTQSK 225
DB 176 KKVTAQELDIKVRTKLNAYKLYDRMTSDVQKGYIKFHSHEKESFYVDLFYIKGNLDP 235
QY 226 KYLMIYKDNETLDSNTSQIEVLT 250
DB 236 QYLQIYNDNKTIDSSDYHIDVYLET 260

RESULT 13
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: yent2

Query Match 25.5%; Score 337; DB 2; Length 136;
Best Local Similarity 49.6%; Pred. No. 4.4e-18;
Matches 67; Conservative 22; Mismatches 38; Indels 8; Gaps 2;
QY 125 RSACIYGGVTNHEGHNH-----EIPKKIIVKVSIDGIQSLSFDIETNKKMVTVAQELDYK 178
DB 2 KKTVMYGGVTEHDGNQIDKNNSTDNHNLIKVYENERNLSLDFIPTNKKNTAQEIDYK 61
QY 179 VRKYLTDNKKQLYNGPSKYETGYIKFIPKNKESFWDFPFPE--PEFTQSKYLMYKDNET 236
DB 62 VRNYLLKHKNLNLYEFNSSPYETGYIKFIEGSHSFYDLMPESGKRFYPTKYLIIYNDNKT 121
QY 237 LDSNTSQIEVLT 251
DB 122 VESKSINVEVLT 136

RESULT 14
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89984
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q99SU3; GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: sep
C;Superfamily: enterotoxin B

Query Match 25.4%; Score 336; DB 2; Length 260;
Matches 96; Conservative 42; Mismatches 107; Indels 20; Gaps 9;

A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 41.5%; Score 549; DB 2; Length 266;
Best Local Similarity 44.1%; Pred. No. 2.3e-33;
Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;

QY 11 MVP-FVLVTFGLTISQEVFAQODPPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV 68
Db 12 LIFALILVLFPTPNVLAE---SQDPDTPDELHKSEFTGTGNMKNKLYDDHYVSATKVS 68

QY 69 DQLRSHDLIYNVSG---PNYDKLKTQEMATLFDKKNVDIYGVEYHLCYL--ENA 123
Db 69 DKFLAHDLIYINSDKKLKNYDKVKTLLNEDLAKYKDEVDVYGSNYCYFSSKDNV 128

QY 124 ER----SACIYGGVTNHEGNHLEIP--KTIWVKVSDIGIQSLSFDIETNKNMVTQAELDY 177
Db 129 GKVTGGKTCMYGGITKHEGNHFNQNLQNLVIRVENKNTISFEVQTDKKSVTABELDI 188

QY 178 KVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPPEP--BFTOSKYLMIYKDNE 235
Db 189 KARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMWMPAPGDKFDQSKYLMYNDNK 248

QY 236 TLDSNTSQIEVLVTTK 251
Db 249 TVDSKSVKIEVHLTTK 264

RESULT 9
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness b
A;Reference number: S06356; MUID:88038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567
R;Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75,'IL',78-176,'N',178-266 <SCH>
C;Genetics:
A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

Query Match 41.5%; Score 548; DB 1; Length 266;
Best Local Similarity 44.5%; Pred. No. 2.7e-33;
Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

A;Residues: 28-66 <BOH2>
R;Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A;Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th
A;Reference number: A33866; MUID:89327174; PMID:2473979
A;Accession: A33866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-266 <COU>
A;Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C;Genetics:
A;Gene: entC2
C;Superfamily: enterotoxin B
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 41.5%; Score 549; DB 2; Length 266;
Best Local Similarity 44.1%; Pred. No. 2.3e-33;
Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;

QY 11 MVP-FVLVTFGLTISQEVFAQODPPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSV 68
Db 12 LIFALILVLFPTPNVLAE---SQDPDTPDELHKSEFTGTGNMKNKLYDDHYVSATKVS 68

QY 69 DQLRSHDLIYNVSG---PNYDKLKTQEMATLFDKKNVDIYGVEYHLCYL--ENA 123
Db 69 DKFLAHDLIYINSDKKLKNYDKVKTLLNEDLAKYKDEVDVYGSNYCYFSSKDNV 128

QY 124 ER----SACIYGGVTNHEGNHLEIP--KTIWVKVSDIGIQSLSFDIETNKNMVTQAELDY 177
Db 129 GKVTGGKTCMYGGITKHEGNHFNQNLQNLVIRVENKNTISFEVQTDKKSVTABELDI 188

QY 178 KVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPPEP--BFTOSKYLMIYKDNE 235
Db 189 KARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMWMPAPGDKFDQSKYLMYNDNK 248

QY 236 TLDSNTSQIEVLVTTK 251
Db 249 TVDSKSVKIEVHLTTK 264

RESULT 10
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: UNIPROT:O85382; GB:BA000018; PID:g13701617; PIDN:BAB42910.1; GSPDB:5
A;Experimental source: strain N315
C;Genetics:
A;Gene: seg
C;Superfamily: enterotoxin B

Query Match 36.4%; Score 481; DB 2; Length 258;
Best Local Similarity 40.7%; Pred. No. 2.3e-28;
Matches 105; Conservative 46; Mismatches 91; Indels 16; Gaps 5;

QY 8 LKQWFFVLVTFGLTISQEVFAQODPP--SQLHRSSLVKN---LQNIYFLYEGDPVT 61
Db 1 MKKLTVIIILILEIVFHNMYVNAQPPKLDLKNVSDYKKNKGTGMGNMNLVTSPPVE 60

QY 62 HENVKSDQLRSHDLIYNVSGPNYDKLKTQEMATLFDKKNVDIYGVEYHLCYLCE 121
Db 61 GRGVINSQFUSHDLIFPIEYKSEVTELENTLANNYKDKKIDFVGVPFYTCIIIPK 120

QY 122 NAE-----RSACIYGGVTNHEGNHLEIPKKIIVKVSIDIGIQSLSFDIETNKNMVTQAEL 175
Db 121 SEPDINQFGCCWYGGITFNSSEN-ERDKLITVQVTDNRQSLGFTITNKNMVTIQL 179

QY 176 DYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPPEPE---FTOSKYLMIYK 232
Db 180 DYKARHVLTKKKLYEFDGSAPESGYIKFTEKNNTSFWFDLPKKELVFPVFPKFLNIYG 239

QY 233 DNETLDSNTSQIEVLVTT 250
Db 240 DNKVVDSKSIKMEVFLNT 257

RESULT 11
A33953
enterotoxin D precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus

QY 181 KYLTQNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPETQSKYLYMKDNETLDSN 240
DB 180 KYLTQNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPETQSKYLYMKDNETLDSN 239
QY 241 TSQIEVLYLTTK 251
DB 240 TSQIEVLYLTTK 250

RESULT 6
ENSB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: S27360; S27365; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029; PMID:3957869
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <ON>
A:Cross-references: UNIPROT:P01552; EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g1530
A:Experimental source: strain S6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
A:Reference number: A92065; MUID:71007902; PMID:5470821
A:Accession: A92065
A:Molecule type: protein
A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',
A:Experimental source: strain S-6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
A:Reference number: A92064; MUID:71007901; PMID:5470820
A:Contents: annotation; chymotryptic peptides
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
A:Reference number: A92063; MUID:71007900; PMID:5470819
A:Contents: annotation; tryptic peptides
R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792; PMID:4953912
A:Contents: annotation; biological source of protein
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A:Reference number: S27240; MUID:93049338; PMID:1425690
A:Accession: S27240
A:Molecule type: protein
A:Residues: 28-42; 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin B #status experimental <MAT>
F:120-140/Disulfide bonds: #status experimental

Query Match 43.6%; Score 576.5; DB 1; Length 266;
Best Local Similarity 48.2%; Pred. No. 2.1e-35;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS-QEVFA--QODPDPSQLHRSLLVKNL-QNIYFLYEGDPVTHENVKSVQ 70
DB 11 ILIFALILVISTPNVLAESQDPDPDLHKSSEFTGMNKNKLYLDHVSATKVKSVQ 70

QY 71 LRSHDLIYNVSG---NYDKLTELKNQEMATLFDKNVDIYGVYHYHLCYCENA--- 123
DB 71 FLFDLIYSIKDTLGNVDNRVFEFKDKLADKKYKVDVFGANYYYQCYFSKKTNDIN 130

QY 124 -----ESACIYGGVTHNHNLEIPKKIVKVSIDGISOLESFIEDTNKKQVTAQELDYK 178
DB 131 SHQTDKRTCMYGGVTEHNGQLDKYSITVRVFEDGKNLLSFDVQTNKKVTAQELDYL 190
QY 179 VRKLYTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPETQSKYLYMKDNET 236
DB 191 TRHYLVKNKLYEFNNSPYETGYIKFI-ENESFWYDMMPAPGDKFDQSKYLYMNDNKM 249
QY 237 LDSNTSQIEVLYLTTK 251
DB 250 VDSKDVKIEVLYLTTK 264

RESULT 7

S11885
enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S11885
R:Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A:Reference number: S11885; MUID:90220508; PMID:2325627
A:Accession: S11885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <OV>
A:Cross-references: UNIPROT:P23313; GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571
C:Superfamily: enterotoxin B

Query Match 41.7%; Score 551.5; DB 2; Length 266;
Best Local Similarity 46.1%; Pred. No. 1.5e-33;
Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps 8;

QY 15 VLVTFLGLTIS-QEVFAQODPD--PSQLHRS-LVKNLQNIYFLYEGDPVTHENVKSVQ 70
DB 11 ILIFALILVISTPNVLAESQDPDPDLHKSSEFTGMNKNKLYLDHVSATKVKSVQ 70

QY 71 LRSHDLIYNVSG---PNYDKLTELKNQEMATLFDKNVDIYGVYHYHLCYC--ENAE 125
DB 71 FLAHDLIYINISDKLKNYDKVKTLLNEDLAKKYKDEVVDVVGSYNYVYVYSSKDNVQK 130

QY 126 ---SACIYGGVTHNHNLEIP--KKIWKVSIIDGISOLESFIEDTNKKQVTAQELDYK 179
DB 131 VTGKTCMIGITKEGHNHFNQNLQNVLRVYENKRNITISFEVQTKKSVTAQELDIKA 190

QY 180 RYKLYTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPETQSKYLYMKDNETL 237
DB 191 RNFLINKKNLYEFNNSPYETGYIKFIENNGNTFTWDMMPAPGDKFDQSKYLYMNDNKT 250

QY 238 DSNTSQIEVLYLTTK 251
DB 251 DSKSVKIEVLYLTTK 264

RESULT 8

A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: UNIPROT:P34071
A:Accession: B60114
A:Molecule type: protein

A;Residues: 1-236 <NEA>
A;Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A;Experimental source: strain MGAS251 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18788
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEZ>
A;Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A;Experimental source: strain MGAS256 isolate California unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEY>
A;Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A;Experimental source: strain MGAS285 isolate Colorado unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA2>
A;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
Query Match 93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 5.4e-84;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
DB 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 60
QY 69 DQLRSHDLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCEAERSAC 128
DB 61 DQLLSDHLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCEAERSAC 120
QY 129 IYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 188
DB 121 IYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 180
QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 236
RESULT 4
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes
A;Variety: strain MGAS262 isolate California

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S18789
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene enco
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18789
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEL>
A;Cross-references: UNIPROT:Q54696; EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g4730
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>
Query Match 83.9%; Score 1109; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 9.1e-75;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
DB 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 60
QY 69 DQLRSHDLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCEAERSAC 128
DB 61 DQLLSDHLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCEAERSAC 120
QY 129 IYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 188
DB 121 IYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVRKYLTDNKQ 180
QY 189 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 244
DB 181 LYTNGPSKYETGYIKFIPKNKESFWDFPPEPFTQSKYLMYKONETLDSNTSQI 236
RESULT 5
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; SPE type A (speA)
C;Species: Streptococcus sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to St
A;Reference number: A26152; MUID:86284313; PMID:3526093
A;Accession: A26152
A;Molecule type: DNA
A;Residues: 1-250 <JOH>
A;Cross-references: UNIPROT:P08095
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
Query Match 81.4%; Score 1075.5; DB 1; Length 250;
Best Local Similarity 83.7%; Pred. No. 2.9e-72;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;
QY 1 MNNKVKLVKQVFFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 60
DB 1 MNNKVKLVKQVFFVLTFLGLTILPKGICSTRPSPQSLQSLRSLVKTFKIYIFFRVTLV 60
QY 61 THENVKSVDQLRSHDLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCE 120
DB 61 THENVKSVDQLLSDHLIYVSGPNYDKLTTELKNQEMATLTKDNVDIYGVVEYHLCYLCE 120
QY 121 ENAERSACIYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNHLEIPKKIYVVKVSIQSLSDIETNKKMVTQAQELDYKVR 179

A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18797
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NEH>
A;Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-228 <NES>
A;Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
C;Gene: speA; speA1
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-251/Product: exotoxin type A #status predicted <MAT>

Query Match	99.5%;	Score 1315;	DB 1;	Length 251;
Best Local Similarity	99.8%;	Pred. No. 6.1e-90;		
Matches 250;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 1 MENNKKVLKQWFFVLVTFGLTISQEVFAQQDPDPQSLHRSLSVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKQWFFVLVTFGLTISQEVFAQQDPDPQSLHRSLSVKNLQNIYFLYEGDPV 60

Qy 61 THENVKSVDQLRSHDLIYVNSGPNYDKLTTELKNQEMATLFDKKNVDIYGEVYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYVNSGPNYDKLTTELKNQEMATLFDKKNVDIYGEVYHLCYLC 120

Qy 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGTQISLFDIETNKKMVTAGLDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGTQISLFDIETNKKMVTAGLDYKVR 180

Qy 181 KYLTDNKQLYNTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLIYKDNETLDSN 240
Db 181 KYLTDNKQLYNTGSPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLIYKDNETLDSN 240

Qy 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 2
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isolate
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18783; S18793; S18794; S18801; S18798
R;Nelson, K.; Schlievert, P.M.; Selaender, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEL>
A;Cross-references: EMBL:X61568; NID:g47289; PIDN:CAA43766.1; PID:g47290
A;Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage

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OM protein - protein search, using sw model

Run on: September 17, 2005, 01:00:14 ; Search time 18.153 Seconds
(without alignments)
1330.382 Million cell updates/sec

Title: US-10-002-784A-16
Perfect score: 1322
Sequence: 1 MNNKKVLKXWFFVLVTEL.....KDNETLDSNTSQIEVYLTK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	99.5	231	1 S29659	exotoxin type A pr
2	1239	93.7	236	2 S18783	exotoxin type A pr
3	1234	93.3	236	2 S18786	exotoxin type A pr
4	1109	83.9	236	2 S18789	exotoxin A precurs
5	1075.5	81.4	250	1 A26152	streptococcal pyro
6	576.5	43.6	266	1 ENSAB6	enterotoxin B prec
7	551.5	41.7	286	2 S11885	enterotoxin C3 - S
8	549	41.5	266	2 A60114	enterotoxin C-2 pr
9	548	41.5	266	1 ENSAC1	enterotoxin C-1 pr
10	481	36.4	258	2 G89968	extracellular ente
11	340	25.7	258	2 A33953	enterotoxin D prec
12	338	25.6	260	2 E89969	enterotoxin SeO fi
13	337	25.5	136	2 A89969	enterotoxin YENT2
14	336	25.4	260	2 C89984	enterotoxin SeN fi
15	311.5	23.6	258	2 H89968	enterotoxin SeN fi
16	308	23.3	257	2 A28179	enterotoxin E prec
17	307	23.2	257	2 A28664	enterotoxin A prec
18	305.5	23.1	240	2 G89991	extracellular ente
19	264	20.0	239	2 D89969	enterotoxin SEM fi
20	251.5	19.0	242	2 C89969	extracellular ente
21	211	16.0	235	2 A30509	exotoxin C precurs
22	174	13.2	133	2 B89969	exotoxin Yent1
23	129.5	9.8	221	2 D89807	exotoxin 11 [import
24	128	9.7	227	2 A89942	hypothetical prote
25	125	9.5	137	2 C89808	exotoxin 15 [import
26	114	8.6	232	2 F89807	exotoxin 13 [import
27	114	8.6	234	2 C89807	exotoxin 10 [import
28	111	8.4	234	2 B89992	toxic shock syndro
29	111	8.4	292	2 B89807	exotoxin 9 [import

30	109.5	8.3	825	2	H82885	hypothetical prote
31	109	8.2	234	1	XCSAS1	toxic shock syndro
32	108.5	8.2	231	2	H89806	exotoxin 7 [import
33	108.5	8.2	596	2	E96935	FUSION, methionine
34	108	8.2	434	2	T28342	ORF MSV181 hypothe
35	108	8.2	493	2	G90604	hypothetical prote
36	105.5	8.0	1790	2	S67593	transport protein
37	105	7.9	770	2	B48910	desmocollin 1b pre
38	105	7.9	824	2	A48910	desmocollin 1a pre
39	105	7.9	890	2	I37281	Dscib precursor -
40	105	7.9	894	2	I37282	Dscib precursor -
41	104.5	7.9	1367	2	T18466	hypothetical prote
42	104.5	7.9	1856	2	C95008	immunoglobulin A1
43	103.5	7.8	241	2	B89888	hypothetical prote
44	103.5	7.8	396	2	S09627	prnC protein - Esc
45	103	7.8	235	2	C97252	probable membrane

ALIGNMENTS

RESULT 1

S29659

exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12

N:Alternate names: erythrogenic toxin; scarlet fever toxin

C:Species: Streptococcus pyogenes phage T12

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999

C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

R:Weeks, C.R.; Ferretti, J.J.

Infect. Immun. 52, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin)

A:Reference number: S29659; MUID:86166804; PMID:3514452

A:Accession: S29659

A:Molecule type: DNA

A:Residues: 1-251 <WE>

A:Cross-references: GB:U40453; EMBL:X61560; NID:gl877426; PIDN:AA43758.1; PID:gl877430

R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene enco

A:Reference number: S18782; MUID:92044323; PMID:1940804

A:Accession: S18782

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NE>

A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288

A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigne

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18784

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292

A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassign

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18785

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEZ>

A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294

A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned p

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18791

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NE>

A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310

A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18796

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEO>

A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

Db 250 VDSKDVKIEVLTTK 264

RESULT 15
US-09-751-708A-10
; Sequence 10, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-10

Query Match 43.6%; Score 576.5; DB 10; Length 266;
Best Local Similarity 48.2%; Pred. No. 1.3e-41;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTIS-QEVFA--QQDPDPSQLHSSLVKNL-QNIYELYEGDPVTHENVKSDQ 70
Db 11 ILIFALLVLTSTENVLAESQDPKPDDELHKSSFTGLMENMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP--NYDKLTTELKNQEMATLFDKNVDIYGVVYHYLCYCENA---- 123
Db 71 FLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDYVDVFCGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTNHEGNHLEIPKKIVVKVSIIDGIOSLSFDIETNKQMTAQELDYK 178
Db 131 SHQTKRKTCMYGGVTEHNGNQLDKYRSITRVVFEDGKNLLSPDVQTNKKKVTQAELDYL 190

QY 179 VRKYLTDNKOLYNGPSKYETGYIKETPKNKESFWDFPPEP--EFTQSKYLMYKDNET 236
Db 191 TRHYLVKNKGLYEFNNSPYETGYIKFI-ENENSFWYDMMPAPGDKFDQSKYLMYNDNKM 249

QY 237 LDSNTSQIEVLTTK 251
Db 250 VDSKDVKIEVLTTK 264

Search completed: September 17, 2005, 01:05:39
Job time : 79.8484 secs

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; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-937-758A-20

Query Match      81.4%; Score 1075.5; DB 17; Length 250;
Best Local Similarity 83.7%; Pred. No. 6.7e-85;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

QY 1 MENNKKVLKMMFFVFLVLTGLTISQEVFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKMMFFVFLVLTGLTILPKGICSTRPKSPQQRSLNLTFKIYIFFMRVTLV 60

QY 61 THENKVSVDQLRSHDLIYNVSGPNVDKLTTELKNOEMATLFDKKNVDIYGYEYHLCYLC 120
Db 61 THENKVSVDQLRSHDLIYNVSGPNVDKLTTELKNOEMATLFDKKNVDIYGYEYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQLSFDIETNKKMVTAAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQLSFDIETNKKMVTAAQELDYKVR 180

QY 181 KYLTNKKQLYTNGSPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTNKKQLYTNGSPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
Db 240 TSQIEVYLTTK 250
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RESULT 13
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication NO. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Potter, Terence A.
; Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match      44.5%; Score 588; DB 15; Length 255;
Best Local Similarity 47.2%; Pred. No. 1.2e-42;
Matches 119; Conservative 41; Mismatches 76; Indels 16; Gaps 5;

QY 15 VLVTFLGLTISQEVFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRS 73
Db 3 MITNLRLITIGNSMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLY 62

QY 74 HDLIYNVSGP---NYDKLTTELKNOEMATLFDKKNVDIYGYEYHLCYCENA----- 123
Db 63 FDLIYSIKDITKLGNYDNVRVEFKNLADKDKYDVDFGANYYYQCYFSKKTNDINSHQ 122

QY 124 --ERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQLSFDIETNKKMVTAAQELDYKVR 181
Db 123 TDKRKTCMYGGVTEHNGQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDYLTRH 182

QY 182 YLTNKKQLYTNGSPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNETLDS 239
Db 183 YLVNKKLYEFNNSPYETGIYKFI-ENENSWYDMWPAPGDKFDQSKYLMYNDNMKVDS 241

QY 240 NTSQIEVYLTTK 251
Db 242 KDKVIEVYLTTK 253

RESULT 14
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match      43.6%; Score 576.5; DB 9; Length 266;
Best Local Similarity 48.2%; Pred. No. 1.3e-41;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFLGLTISQEVFA--QQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQD 70
Db 11 ILIPALILVISTPNVLAESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQ 70

QY 71 LRSHDLIYNVSGP---NYDKLTTELKNOEMATLFDKKNVDIYGYEYHLCYCENA---- 123
Db 71 FLYFDLIYSIKDITKLGNYDNVRVEFKNLADKDKYDVDFGANYYYQCYFSKKTNDIN 130

QY 124 -----ERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQLSFDIETNKKMVTAAQELDYK 178
Db 131 SHQTDKRRKTCMYGGVTEHNGQLDKYRSITVRVFDGKNLLSFDVQTNKKVTAQELDY 190

QY 179 VRKYLTNKKQLYTNGSPSKYETGIYKFIKPKNKESFWDFPFPEPTQSKYLMYKDNET 236
Db 191 TRHYLVNKKLYEFNNSPYETGIYKFI-ENENSWYDMWPAPGDKFDQSKYLMYNDNMKN 249

QY 237 LDSNTSQIEVYLTTK 251
Db 237 LDSNTSQIEVYLTTK 251
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; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-308-830-13

Query Match      98.9%; Score 1308; DB 9; Length 251;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENNKKVLKMMFFVLVTLGLTISQEVFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKMMFFVLVTLGLTISQEVFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTKTELKQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTKTELKQEMATLFDKKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGVVTHNEGNHLEIPKIVVKSIDGQSLSFDIETNKKQWTAQELDYKVR 180
DB 121 ENAERSACIYGVVTHNEGNHLEIPKIVVKSIDGQSLSFDIETNKKQWTAQELDYKVR 180
QY 181 KYLTNKKQWTAQELDYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 240
DB 181 KYLTNKKQWTAQELDYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 7
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match      85.9%; Score 1136; DB 14; Length 220;
Best Local Similarity 98.2%; Pred. No. 3.2e-90;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 31 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 90
DB 2 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYNVSGPNYDKLKT 61
QY 91 ELKQEMATLFDKKNVDIYGVYHLCYLCENASRSACIYGVVTHNEGNHLEIPKIVVK 150
DB 62 ELKQEMATLFDKKNVDIYGVYHLCYLCENASRSACI -GGVTNREGNHLEIPKIVVK 120
QY 151 VSIDGQSLSFDIETNKKQWTAQELDYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 210
DB 121 VSIDGQSLSFDIETNKKQWTAQELDYKVRKYLTDNKLQYNGPSKYETGVIKFIKPKNKE 180
QY 211 SFWDFPFPEPTQSKYLMYKDNETLDSNTSQIEVYLTTK 251
DB 181 SFWDFPFPEPTQSKYLMYKDNETLDSNT -QIEVYLTTK 220

RESULT 9
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
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Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSFQIETNKKMVTQAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 4
US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-163

Query Match 99.5%; Score 1315; DB 16; Length 251;
Best Local Similarity 99.8%; Pred. No. 1.2e-105;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
Db 61 THENVKVDQLRSHDLIYNVSGPNYDKLTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSFQIETNKKMVTQAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSFQIETNKKMVTQAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 5
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
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; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match 98.9%; Score 1308; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 4.8e-105;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLRSSLVKNLQNIYFLYEGDPV 60
Db 1 MENKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKVDQLRSHDLIYNVSGPNYDKLTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
Db 61 THENVKVDQLRSHDLIYNVSGPNYDKLTELKNQEMATLFDKKNVDIYGVYYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSFQIETNKKMVTQAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSFQIETNKKMVTQAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 6
US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 100.0%; Score 1322; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDVKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDVKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match 100.0%; Score 1322; DB 14; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDVKVR 180
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DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDVKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 3
US-10-767-687-16
; Sequence 16, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRCM -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match 100.0%; Score 1322; DB 17; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.9e-106;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MENNKKVLKQVFFVLVTLFLGLTISQEVFAQQDDPPSOLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDVKVR 180
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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: September 17, 2005, 00:44:58 ; Search time 77.8484 Seconds
(without alignments)
1305.574 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322
Sequence: 1 MENNKVLKMWFFVLVTF...KDNFTLDSNTSIEVILTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322	100.0	251	8	US-08-882-431-16
2	1322	100.0	251	14	US-10-002-784A-16
3	1322	100.0	251	17	US-10-002-784A-16
4	1315	99.5	251	16	US-10-002-784A-16
5	1308	98.9	251	8	US-08-882-431-16
6	1308	98.9	251	9	US-09-308-830-13
7	1136	85.9	220	14	US-10-002-784A-26
8	1136	85.9	468	14	US-10-002-784A-27
9	1075.5	81.4	250	9	US-09-870-759-20
10	1075.5	81.4	250	10	US-09-751-708A-20
11	1075.5	81.4	250	16	US-10-428-817A-16

12	1075.5	81.4	250	17	US-10-937-758A-20
13	588	44.5	255	15	US-10-354-948-2
14	576.5	43.6	266	9	US-09-870-759-10
15	576.5	43.6	266	10	US-09-751-708A-10
16	576.5	43.6	266	16	US-10-428-817A-6
17	576.5	43.6	266	17	US-10-937-758A-10
18	576	43.6	239	9	US-09-150-947B-12
19	576	43.6	239	14	US-10-172-425B-12
20	575	43.5	266	14	US-10-151-336-8
21	574	43.4	238	16	US-10-428-817A-183
22	567.5	42.9	266	14	US-10-002-784A-6
23	567.5	42.9	266	17	US-10-767-687-6
24	563	42.6	239	14	US-10-002-784A-10
25	563	42.6	239	17	US-10-767-687-10
26	558.5	42.2	266	14	US-10-002-784A-8
27	558.5	42.2	266	17	US-10-767-687-8
28	558	42.2	239	8	US-08-882-431-10
29	553	41.8	266	8	US-08-882-431-14
30	553	41.8	266	14	US-10-002-784A-14
31	553	41.8	266	17	US-10-767-687-14
32	551.5	41.7	266	16	US-10-428-817A-186
33	549	41.5	265	8	US-08-882-431-6
34	548	41.5	266	9	US-09-870-759-12
35	548	41.5	266	10	US-09-751-708A-12
36	548	41.5	266	16	US-10-428-817A-8
37	548	41.5	266	17	US-10-937-758A-12
38	547	41.4	240	17	US-10-923-324-4
39	545	41.2	239	16	US-10-428-817A-185
40	544	41.1	240	17	US-10-923-324-1
41	542	41.0	265	8	US-08-882-431-8
42	536	40.5	240	17	US-10-923-324-5
43	535	40.5	240	17	US-10-923-324-3
44	533	40.3	240	17	US-10-923-324-6
45	532	40.2	240	17	US-10-923-324-2

ALIGNMENTS

RESULT 1
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army WMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:

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XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX PT non-lethal - used in vaccine composition for treatment of cancer and
XX PT streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX CC animals against wild type SPE-A and to treat cancer and streptococcal
XX CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX CC myositis, fascitis and liver damage. The neutralising Ab is preferably
XX CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX CC especially useful for treating T cell lymphomas, and ovarian and uterine
XX CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX CC cell lymphoma cells. N.B. Sequence not given in the specification, but
XX CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
SQ
Query Match 98.2%; Score 1298; DB 2; Length 251;
Best Local Similarity 98.8%; Pred. NO. 4.9e-109;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 MNNKKVLKMMVFFVLVTLGLTISOEVFAQQDDPPSQLRSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTQELKNQEMATLFDKNVDIYGVYHLCYL 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTQELKNQEMATLFDKNVDIYGVYHLCYL 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTQAQELDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSPDIETNKKMVTQAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251
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Search completed: September 17, 2005, 01:09:41
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Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 DB 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQDIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVVYHLCYLC 120
 DB 61 THENVKSVDQLSHHLIYNVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVVYHLCYLC 120
 QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDYKVR 180
 DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDYKVR 180
 QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
 DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVLYTTK 251
 DB 241 TSQIEVLYTTK 251

RESULT 14
 AAW12148
 ID AAW12148 standard; protein; 251 AA.
 AC AAW12148;
 XX
 DT 04-NOV-1997 (first entry)
 XX
 DE Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157B.
 XX
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 OS Streptococcus pyogenes.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..30 /label= sig_peptide
 FT Peptide 31..251 /label= mat_peptide
 FT Misc-difference 50 /note= "wild type Asn replaced by Asp"
 FT Misc-difference 187 /note= "wild type Lys replaced by Glu"
 FT
 XX WO9640930-A1.
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US010252.
 XX
 XX 07-JUN-1995; 95US-00480261.
 XX
 XX (MINU) UNIV MINNESOTA.
 XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX WPI; 1997-099936/09.
 XX
 XX Mutant SPE-A toxin with at least one amino acid change is substantially
 PT non-lethal - used in vaccine composition for treatment of cancer and
 FT streptococcal toxic shock syndrome etc.
 XX
 XX Claim 5; Page; 102pp; English.
 XX
 XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal

CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
 CC animals against wild type SPE-A and to treat cancer and streptococcal
 CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
 CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
 CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
 CC myositis, fascitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and uterine
 CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
 CC cell lymphoma cells. N.B. Sequence not given in the specification, but
 CC constructed using the wild type SPE-A sequence given on pages 77-79
 XX
 SQ Sequence 251 AA;

Query Match 98.3%; Score 1299; DB 2; Length 251;
 Best Local Similarity 98.4%; Pred. No. 3.9e-109;
 Matches 247; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPV 60
 DB 1 MNNKKVLKQWFFVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQDIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVVYHLCYLC 120
 DB 61 THENVKSVDQLSHHLIYNVSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVVYHLCYLC 120
 QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDYKVR 180
 DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSDIGIQSLSFDIETNKKMVTAAQELDYKVR 180
 QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
 DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVLYTTK 251
 DB 241 TSQIEVLYTTK 251

RESULT 15
 AAW12153
 ID AAW12153 standard; protein; 251 AA.
 XX
 AC AAW12153;
 XX
 DT 04-NOV-1997 (first entry)
 XX
 DE Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
 XX
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 OS Streptococcus pyogenes.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..30 /label= sig_peptide
 FT Peptide 31..251 /label= mat_peptide
 FT Misc-difference 120 /note= "wild type Cys replaced by Ser"
 FT
 XX WO9640930-A1.
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US010252.
 XX
 XX 07-JUN-1995; 95US-00480261.


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XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
DE Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW Streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 46
FT /note= "wild type Lys replaced by Asn"
XX
XX WO9640930-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fascitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
XX
XX Query Match 98.6%; Score 1303; DB 2; Length 251;
XX Best Local Similarity 98.8%; Pred. No. 1.7e-109;
XX Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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XX 1 MENNKKVLKMWPFVLVTLFGLTISQEVFAQQDPDSQLHRSLSVKNLQNIYFLYEGDPV 60
XX
XX 61 THENVKVSDQLRSHDLIYVNSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVYHLCYLC 120
XX
XX 61 THENVKVSDQLRSHDLIYVNSGPNYDKLKTTELKNQEMATLFDKKNVDIYGVYHLCYLC 120
XX
XX 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDGISOISLFDIETNKKMWTAQELDYKVR 180
XX
XX 121 ENAERSACIYGGVTNHEGNHLEIPKKIIVVKVSIIDGISOISLFDIETNKKMWTAQELDYKVR 180
XX
QY 181 KYLTNDKQLYTNNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSN 240
DB 181 KYLTNDKQLYTNNGPSKYETGYIKFIPKNKESFWDFPEPEFTOSKYLMIYKDNETLDSN 240
QY 241 TSQIEVLVLTTK 251
DB 241 TSQIEVLVLTTK 251
RESULT 13
AAW12147
ID AAW12147 standard; protein; 251 AA.
XX
XX AAW12147;
AC
XX
XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Aasn20Aasp.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW Streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX Streptococcus pyogenes.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..30
XX /label= sig_peptide
XX Peptide 31..251
XX /label= mat_peptide
XX Misc-difference 50
XX /note= "wild type Asn replaced by Asp"
XX
XX WO9640930-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX (MINU ) UNIV MINNESOTA.
XX
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fascitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
XX
XX Query Match 98.6%; Score 1303; DB 2; Length 251;
XX Best Local Similarity 98.8%; Pred. No. 1.7e-109;
```


CC and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes
 CC neutralising antibodies (Ab) to be produced, which may be used to
 CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal
 CC infection, myositis, fascitis and liver damage. The neutralising Ab is
 CC preferably administered in conjunction with antibiotic therapy. The
 CC mutant SPE-A is especially useful for treating T cell lymphomas, and
 CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
 CC selectively toxic to T cell lymphoma cells
 XX
 SQ Sequence 251 AA;

Query Match 98.9%; Score 1308; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 6e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
 DB 1 MENNKKVLKQVFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGYEYHLCYLC 120
 DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGYEYHLCYLC 120
 QY 121 ENAERSACIYGGVTHNHEGHNLEIPKKIYVVKVSIQSLSPDIETNKKMVTQAQLDYKVR 180
 DB 121 ENAERSACIYGGVTHNHEGHNLEIPKKIYVVKVSIQSLSPDIETNKKMVTQAQLDYKVR 180
 QY 181 KYLTNDKQLYTNQPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 DB 181 KYLTNDKQLYTNQPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVYLTTK 251
 DB 241 TSQIEVYLTTK 251

RESULT 9

AAW59780
 ID AAW59780 standard; protein; 251 AA.

AC AAW59780;

DT 12-OCT-1998 (first entry)

XX Amino acid sequence of Streptococcus pyogenes exotoxin A.

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.

XX Streptococcus pyogenes.

XX WO9824911-A2.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US022228.

XX 06-DEC-1996; 96US-0032930P.

XX (MINU) UNIV MINNESOTA.

XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

XX WPI; 1998-333330/29.

XX N-PSDB; AAV41593.

XX New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or
 PT treatment of streptococcal infection or toxic shock syndrome.

XX Disclosure; Fig 3; 95pp; English.

XX

CC This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1
 CC aa change and is nonlethal compared with a protein to wild type SPE-A
 CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used in
 CC vaccines and therapeutics to generate a protective immune response
 CC against streptococcal infection. They can be used to protect against the
 CC development of streptococcal toxic shock syndrome (STSS). In addition,
 CC the toxins can be used for treating animals with symptoms of
 CC streptococcal infection or STSS and in methods for stimulating T cell
 CC proliferation and in the treatment of cancer. In particular they can be
 CC used for treating T cell lymphomas, and ovarian and uterine cancer
 XX
 SQ Sequence 251 AA;

Query Match 98.9%; Score 1308; DB 2; Length 251;
 Best Local Similarity 99.2%; Pred. No. 6e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENNKKVLKQVFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
 DB 1 MENNKKVLKQVFFVLTFLGLTISQEVFAQDDPPSOLHRSSLVKNLQNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGYEYHLCYLC 120
 DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFDKKNVDIYGYEYHLCYLC 120
 QY 121 ENAERSACIYGGVTHNHEGHNLEIPKKIYVVKVSIQSLSPDIETNKKMVTQAQLDYKVR 180
 DB 121 ENAERSACIYGGVTHNHEGHNLEIPKKIYVVKVSIQSLSPDIETNKKMVTQAQLDYKVR 180
 QY 181 KYLTNDKQLYTNQPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 DB 181 KYLTNDKQLYTNQPSKYETGYIKFIPKNKESFWDFPFPEPTQSKYLMYKDNETLDSN 240
 QY 241 TSQIEVYLTTK 251
 DB 241 TSQIEVYLTTK 251

RESULT 10

AAW12154
 ID AAW12154 standard; protein; 251 AA.

AC AAW12154;

XX 04-NOV-1997 (first entry)

XX Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.

XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.

XX Streptococcus pyogenes.

XX Synthetic.

XX Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= sig_peptide

FT Peptide 31..251
 FT /label= mat_peptide

FT Misc-difference 225
 FT /note= "wild type Ser replaced by Ala"

XX WO9640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010252.

XX

Db 61 THENVKSVDQLASHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVEYHLCYL 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251
RESULT 7
ADF89839
ID ADF89839 standard; protein; 251 AA.
XX
AC ADF89839;
XX
DT 26-FEB-2004 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A (SpEA) sequence.
XX
KW Superantigen; SAg; enterotoxin; cytostatic; gene therapy; cancer;
KW pyrogenic exotoxin; SpE; SpEA.
XX
OS Streptococcus pyogenes.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
XX 08-MAY-2003; 2003WO-US014381.
XX
PF 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
XX WPI; 2004-011997/01.
DR
XX
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 16; 91pp; English.
XX
CC The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Streptococcal pyrogenic exotoxin A (SpEA).
XX
SQ Sequence 251 AA;
XX
Query Match 99.5%; Score 1315; DB 8; Length 251;

Best Local Similarity 99.6%; Pred. No. 1.4e-110;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MENNKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
Db 1 MENNKKVLKKMVFVFLVTLGLTISQEVFAQQDDPPSQLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLASHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVEYHLCYL 120
Db 61 THENVKSVDQLASHDLIYNVSGPNYDKLTTELKNQEMATLFDKKNVDIYGVEYHLCYL 120
QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
Db 121 ENAERSACIYGGVTNHEGHNLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTQAQLDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251
RESULT 8
AAW12097
ID AAW12097 standard; protein; 251 AA.
XX
AC AAW12097;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Peptide /label= mat_peptide
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
DR N-PSDB; AAW12097.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Disclosure; Page 77-79; 102pp; English.
XX
CC The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE
CC -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino
CC acid change, can be derived. The mutant SPE-A can be used to produce
CC vaccines to protect animals against wild type SPE-A and to treat cancer

```
KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
KW gene therapy.
XX
XX Streptococcus pyogenes.
XX
FH Key Location/Qualifiers
FT Peptide 1..29
FT /label= signal_peptide
FT Protein 30..251
FT /note= "S. pyogenes mature SpeA protein"
XX
XX WO2003056015-A1.
XX
XX 10-JUL-2003.
XX
XX 26-NOV-2001; 2001WO-US046540.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX
XX N-PSDB; AAD56771.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Claim 9; Page 130-131; 141pp; English.
XX
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is Streptococcus pyogenes
XX pyrogenic exotoxin A (SpeA) protein. This sequence is used in the
XX invention
XX
XX Sequence 251 AA;
XX
XX Query Match 100.0%; Score 1322; DB 7; Length 251;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-111;
XX Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNNKKVLKKVFFVLVTLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MNNKKVLKKVFFVLVTLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYHLCYLC 120
Db 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGISLQSLSDIETNKKMVTQAELDVKVR 180
Db 121 ENAERSACIYGGVTNHEGNHLEIPKIVVKVSDIGISLQSLSDIETNKKMVTQAELDVKVR 180
QY 181 KYLTDNKQLYTGSPSKYETGYIKFIPKNKESWFDFFPEPTQSKYLMYKDNETLDSN 240
Db 181 KYLTDNKQLYTGSPSKYETGYIKFIPKNKESWFDFFPEPTQSKYLMYKDNETLDSN 240
QY 241 TSOIEVYLTTK 251
Db 241 TSOIEVYLTTK 251
XX
RESULT 6
ABU62460
ID ABU62460 standard; protein; 251 AA.
XX
AC ABU62460;
XX
```

```
DT 27-AUG-2003 (first entry)
XX Streptococcus pyrogenic toxin a L42A mutant.
DE
XX
XX SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Streptococcus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..30
FT /label= signal_peptide
FT Protein 31..251
FT /label= Mature_SPEa_L42R
FT Misc-difference 72
FT /note= "Wild-type Leu substituted by Ala"
XX
XX US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX
XX Example 13; Page; 68pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection, an
XX antisera isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the L42A (with reference to the mature protein)
XX mutant of SPEa. Note: The present sequence is not shown in the
XX specification but was created by the indexer using the wild-type sequence
XX and the information in the specification
XX
XX Sequence 251 AA;
```

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Query Match 99.5%; Score 1316; DB 7; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.1e-110;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNNKKVLKKVFFVLVTLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
Db 1 MNNKKVLKKVFFVLVTLTISQEVFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFKDKNVDIYGVYHLCYLC 120
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PS Claim 17; Page 34-35; 50pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of streptococcal pyrogenic
CC exotoxin A
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNNKKVLKQWFFVLVTLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVLVTLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTCLKNQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTCLKNQEMATLFDKKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLIYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLIYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251
RESULT 4
ABU62331
ID ABU62331 standard; protein; 251 AA.
AC
XX
XX ABU62331;
XX
DT 27-AUG-2003 (first entry)
XX
DE Streptococcus pyrogenic toxin a L42R mutant.
XX
KW SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Streptococcus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= signal_peptide
FT Protein 31..251
FT Misc-difference 72 /label= Mature_SPEa_L42R
FT /note= "Wild-type Leu substituted by Arg"
XX
XX US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX

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PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1996; 98US-00144776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
DR N-PSDB; ACD28901.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Claim 9; Page 37-38; 69pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the L42R (with reference to the mature protein)
CC mutant of SPEa
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNNKKVLKQWFFVLVTLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKQWFFVLVTLGLTISQEVFAQQDDPSQLHRSLSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTCLKNQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTCLKNQEMATLFDKKNVDIYGVYHLCYLC 120
QY 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMWTAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGNHLEIPKKIVVKVSDIGIQSLSPDIETNKKMWTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLIYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPFPEFTQSKYLIYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251
RESULT 5
AAE37683
ID AAE37683 standard; protein; 251 AA.
XX
XX AAE37683;
XX
XX 06-OCT-2003 (first entry)
XX
XX Streptococcus pyogenes pyrogenic exotoxin A (SPEa) protein.
XX

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CC bacterial infections
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKKNQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKKNQEMATLFDKKNVDIYGVYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIYVVKVSIIDGIQSLSFDIETNKKMVTAAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIYVVKVSIIDGIQSLSFDIETNKKMVTAAQELDYKVR 180

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 2
ID ABB79508
XX ABB79508 standard; protein; 251 AA.
AC ABB79508;
XX
DT 23-SEP-2002 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A vaccine SPEa42.
XX
KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;
KW attenuation; mutant; mutein.
XX
OS Streptococcus pyogenes.
XX Synthetic.
XX
PN US6399332-B1.
XX
PD 04-JUN-2002.
XX
PF 01-SEP-1998; 98US-00144776.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (USSA ) US SEC OF ARMY.
XX
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2002-546281/58.
DR N-PSDB; ABN84229.
XX
XX Novel isolated and purified superantigen toxin DNA fragment which has
PT been genetically altered, useful for producing vaccine for treatment of
PT superantigen toxin-associated bacterial diseases.
XX
XX Disclosure; Col 63-65; 46pp; English.
XX
XX The present sequence is the protein sequence of Streptococcus pyogenes
CC vaccine SPEa42. The vaccine differs from the native SPEa sequence by
CC substitution of the leu-42 residue by Arg. This mutation is expected to
CC disrupt contact between the toxin and the HLA-DR receptor, reducing DRI
CC binding. SPEa42 can be expressed as a recombinant protein in Escherichia
CC coli as a secreted protein or as a cytoplasmic product. No indicators of
CC toxicity have been detected for the purified recombinant protein, and

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CC vaccine studies demonstrate that SPEa42 is highly antigenic, inducing
CC protective immunity in a mouse animal model. The attenuated superantigen
CC can be used to protect against superantigen toxin infections. Methods of
CC producing and using altered superantigen toxins as vaccines, and in
CC diagnosis and therapy, are provided by the invention. A multivalent
CC vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1,
CC TSST-1 and SPEa is predicted to provide protective immunity against the
CC majority of bacterial superantigen toxins
XX
SQ Sequence 251 AA;
Query Match 100.0%; Score 1322; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.3e-111;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPV 60
DB 1 MNNKKVLKKMVFVLTFLGLTISQEVFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPV 60

QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKKNQEMATLFDKKNVDIYGVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTELKKNQEMATLFDKKNVDIYGVYHLCYLC 120

QY 121 ENAERSACIYGGVTNHEGHNLEIPKKIYVVKVSIIDGIQSLSFDIETNKKMVTAAQELDYKVR 180
DB 121 ENAERSACIYGGVTNHEGHNLEIPKKIYVVKVSIIDGIQSLSFDIETNKKMVTAAQELDYKVR 180

QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFPEPEFTQSKYLMYKDNETLDSN 240

QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 3
ABU10088
ID ABU10088 standard; protein; 251 AA.
XX
AC ABU10088;
XX
DT 11-AUG-2003 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A.
XX
KW Pyrogenic exotoxin A; superantigen-associated bacterial infection;
KW superantigen toxin; vaccine.
XX
OS Streptococcus sp.
XX
PN US2003009015-A1.
XX
PD 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
PI
XX WPI; 2003-401542/38.
DR N-PSDB; ACA61184.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or I cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX

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OM protein - protein search, using sw model
Run on: September 17, 2005, 00:47:53 ; Search time 82.0376 Seconds
(without alignments)
1183.322 Million cell updates/sec

Title: US-10-002-784A-16
Perfect score: 1322
Sequence: 1 MNNKVKLVKKWFFVLVTLF.....KDNETLDSNTSQIEVVLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322	100.0	251	3 AAY70109	Streptoco
2	1322	100.0	251	5 ABB79508	Streptoco
3	1322	100.0	251	6 ABU10088	Streptoco
4	1322	100.0	251	7 ABU62331	Streptoco
5	1322	100.0	251	7 AAE37683	Streptoco
6	1316	99.5	251	7 ABU62460	Streptoco
7	1315	99.5	251	8 ADF89839	Streptoco
8	1308	98.9	251	2 AAW12097	Streptoco
9	1308	98.9	251	2 AAW59780	Amino aci
10	1305	98.7	251	2 AAW12154	Streptoco
11	1304	98.6	251	2 AAW12146	Streptoco
12	1303	98.6	251	2 AAW12150	Streptoco
13	1303	98.6	251	2 AAW12147	Streptoco
14	1299	98.3	251	2 AAW12148	Streptoco
15	1298	98.2	251	2 AAW12153	Streptoco
16	1298	98.2	251	2 AAW12151	Streptoco
17	1298	98.2	251	2 AAW12152	Streptoco
18	1293	97.8	251	2 AAW12149	Streptoco
19	1288.5	97.5	250	2 AAW12145	Streptoco
20	1288	97.4	251	2 AAW59798	Amino aci
21	1286	97.3	251	2 AAW59781	Amino aci
22	1170	88.5	221	4 AAB67344	Streptoco
23	1164	88.0	221	2 AAR13209	Streptoco
24	1164	88.0	221	2 AAR45017	Staphyloc
25	1164	88.0	221	5 ABB76240	Staphyloc

26	1136	85.9	220	7 ABU62334	Streptoco
27	1136	85.9	220	7 AAE37687	Streptoco
28	1136	85.9	468	7 ABU62335	SPEA L42R
29	1136	85.9	468	7 AAE37684	Streptoco
30	1131	85.6	220	7 AAE37689	S. pyogen
31	1130	85.5	220	7 AAE37688	S. pyogen
32	1130	85.5	468	7 AAE37691	S. pyogen
33	1075.5	81.4	250	6 ABU79074	S. pyogen
34	1075.5	81.4	250	7 ADF43300	Pyrogenic
35	588	44.5	255	2 AAW06737	Staphyloc
36	576.5	43.6	266	6 ABU79069	S. aureus
37	576.5	43.6	266	7 ABG75015	S. aureus
38	576.5	43.6	266	7 ADF43290	Staphyloc
39	576	43.6	239	2 AAW64647	Synthetic
40	575	43.5	266	3 AAY92319	Plant-opt
41	574.5	43.5	266	7 ABU62454	S. aureus
42	574	43.4	238	8 ADF89825	Staphyloc
43	574	43.4	239	4 AAB67341	Staphyloc
44	574	43.4	239	7 ABG75016	Unidentif
45	574	43.4	239	8 ADL14247	Wild type

ALIGNMENTS

RESULT 1
AAY70109
ID AAY70109 standard; protein; 251 AA.
XX AC AAY70109;
XX AC
XX 05-JUN-2000 (first entry)
XX
DE Streptococcal pyrogenic exotoxin A (SPE-A).
XX
KW Superantigen toxin; SAG; Streptococcal pyrogenic exotoxin A; SPE-A;
KW Antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW Cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;
KW diagnosis; treatment; superantigen-associated bacterial infection.
XX
OS Streptococcus sp.
XX WO200009154-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1998; 98WO-US016766.
XX
XX 13-AUG-1998; 98WO-US016766.
XX (REED-) REED ARMY INST RES WALTER.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX WPI: 2000-224177/19.
XX N-PSDB; AAZ51112.
XX
XX Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.

Example 12; Page 94-95; 118pp; English.

The present amino acid sequence is the Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAG), used for the formulation of SPE-A vaccine SPEA42. The coding region of this SAG toxin is altered by site directed mutagenesis, introducing L42R mutation, that results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPE-A has antibacterial and cytostatic activity. This sequence is useful for the production of SPE-A vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated